

10/594014
IAP9 Rec'd PCT/PTO 25 SEP 2006

SEQUENCE LISTING

<110> DSM IP Assets B.V.
Petrus J.T. Dekker
Marco A. van den Berg

<120> FILAMENTOUS FUNGAL MUTANTS WITH IMPROVED HOMOLOGOUS RECOMBINATION EFFICIENCY

<130> 3663-335 / 24181USWO

<140> US
<141> 2006-09-25

<150> PCT/EP2005/051464
<151> 2005-03-31

<150> EP 04076057.1
<151> 2004-04-02

<160> 23

<170> MS Word

<210> 1
<211> 2284
<212> DNA
<213> Aspergillus niger

<400> 1

atggcggacg	gcaacccaca	tcgggaagat	gaggcggccg	aggaagaaga	ggagattgat	60
gagactgtac	gcaaatttac	ccatgaactt	ggactggAAC	tctggaaactg	acaataagat	120
cagagctaca	aaccagtcaa	agatgcggc	ctcttcgcaa	tcgatgtcag	cgattccatg	180
ttgacgcctc	gcccctcagc	agatcctaag	aaacacaccc	aagaatcacc	caccacggca	240
gcgctcaa	at ggcctatca	cttcatgcaa	caacgaatca	tatcaaatcc	acaagacatg	300
atgggtgttt	tgctgttcgg	gaccaggcg	tccaaagtct	ttgaagaaga	tgaagacagt	360
cggggagacc	tgtcctaccc	caactgctac	ctttcactg	atctggatgt	tccttcggct	420
catgaggtca	aaggacttcg	agcaactggta	gatgatgaag	gagactcaag	ggaggttcta	480
tctccagcga	aagagcaggt	ctctatggca	aacgtcctat	tttgcgccaa	ccagatattc	540
acatccagag	cgc当地attt	cctctcccg	cgtttgtca	tcataaccga	caatgacaac	600
ccccatggtg	atgataaaaac	cctgcggtca	gcggcgactg	tacgtgctaa	ggatctttac	660
gatcttggtg	tcacaattga	gctgtttccg	atctcacgccc	ctgagcatga	gttcaagaac	720
agcaagttct	atgacgtaag	ctatcatact	ctatagcaaa	gtggcagggg	tcgataactca	780
ctacagatac	aaaggatatt	atctacaagt	cattgcccag	cgatccagag	gcgcctgcat	840
atctacaatc	tgattcaaaa	gcggcgactg	cgaccgggaa	cgggatttca	ctcctcaaca	900
cgcttctgtc	cagtattaat	tcgagaacgg	ttccgcgtcg	cactcattt	tcgaacatgc	960
ctttagaact	tggcccagac	ttcagaattt	cgtatcggt	ctatataactc	ttacgaaggc	1020
aagcgcccgc	tagaaactcc	ttcatctggc	tgaacggcga	gaagcctgtg	gtcgcgaaag	1080
gagtgacttc	ccactccgca	gatgatactg	gccggactgt	cgagaaatgg	gagatcagaa	1140
aggcatataa	gttcgggtggc	gaccaagtaa	cctttcgcc	tgatgagcag	aaggcgctta	1200
gggatttcgg	tgagccagta	atccgggtta	ttgggttcaa	gcctatcact	gcgc当地cat	1260
tctggcaaa	cgtcaagcac	ccatatttta	tctatccatc	cgaggaagac	tatgttaggct	1320
cctcgcgagt	atttccgca	ttgcatcaga	ctctttcg	ttccaagaag	atggcactcg	1380
tctggttcat	tgcacgcaag	ggtgctggcc	ccgttctcg	cgctatgatc	gcaggcgaag	1440
aaaagcttga	tgagaatggc	gtacaaaaat	accctcctgg	catgtggatt	cttccctcc	1500
ccttcgcaga	cgatatccgg	cagaaccccg	aaacaacgtt	aatgtcgcc	ccggagtc当地	1560
tgattgatca	gatgcgcgtg	atcgccagc	aactgcagct	gccgaaggga	gtgtacgagc	1620

ctctcaaata	ccccaatcca	tgtaagtcac	ttctgtcttg	cattgctcgt	atacgatgaa	1680
cgagaagctg	acagccccgtg	atcagccctt	caatggcatt	accgcattcct	acaagctctc	1740
gcatttagacg	aagatctccc	cgaaaaacca	gaagacaaaa	ccattccgaa	ataccgccaa	1800
atcgacaagg	taaatccacc	acacccaaca	cgagaaataa	ccctccaggc	gtccaactta	1860
ctgacaattt	caccacagcg	cgccgggtgac	tacgtattat	cctgggcccga	cgaactcgaa	1920
aagcaatacg	ccaaaacccctc	agcagcggcc	cctcgcccaa	ccagcaccct	cgtgaaacga	1980
ggatcaaaag	accgagcaag	cgaaaccgag	gactccaagc	catcgaaaaaa	gatcaagggtt	2040
gaggaagact	ctggaagcct	agaggaggaa	gtccgcaggc	atcacaagaa	gffaacgcta	2100
tccaaggtaa	gccaccacag	gctttctaca	cgtcctcgtg	atggcaaata	tgacatcgta	2160
ttaaccggcg	gttttcttagc	ttacggtcgc	tatcctcaag	gacttcttga	cttccaatgg	2220
acgctcaaata	gccggtaaga	aggcgatct	tattgagcgg	gtagaggagt	tcttggagca	2280
					gtga	2284

<210> 2
 <211> 1947
 <212> DNA
 <213> Aspergillus niger

<400> 2						
atggcggacg	gcaacccaca	tcgggaagat	gaggcggccg	aggaagaaga	ggagattgtat	60
gagactagct	acaaaccagt	caaagatgcg	gtcctcttcg	caatcgatgt	cagcgattcc	120
atgttgcgc	ctcgccccctc	agcagatcct	aagaaacaca	ccaaagaatc	acccaccacg	180
gcagcgctca	aatgcgccta	tcacttcatg	caacaacgaa	tcatatcaaa	tccacaagac	240
atgatgggtg	tttgctgtt	cgggacccag	gcgtccaagt	tctttgaaga	agatgaagac	300
atcgccccgg	acctgtccta	ccccaaactgc	tacctcttca	ctgatctgga	tgttccttcg	360
gctcatgagg	tcaaaggact	tcgagcactg	gtagatgtat	aaggagactc	aaggagggtt	420
ctatctccag	cgaaagagca	ggtctctatg	gcaaacgtcc	tatttgcgc	caaccagata	480
ttcacatcca	gagcgccaaa	tttcctctcc	cggcggttgt	tcatcataac	cgacaatgac	540
aaccccatg	gtgatgataa	aaccctgcgg	tcagcggcga	ctgtacgtgc	taaggatctt	600
tacgatcttgc	gtgtcacaat	ttagctgttt	ccgatctcac	gccctgagca	tgagttcaag	660
aacagcaagt	tctatgactc	attgcccagc	gatccagagg	cgcctgcata	tctacaatct	720
gattcaaaag	cggcgactgc	gaccggggac	gggatttcac	tcctcaacac	gcttctgtcc	780
agtattaatt	cgagaacggt	tccgcgtcgc	actcatttt	cgaacatgcc	tttagaactt	840
ggcccgagact	tcagaatttc	ggtatcgggc	tataactct	tacgaaggca	agcgcccgct	900
agaaactcct	tcatctggct	gaacggcgag	aagcctgtgg	tcgcgaaagg	agtgacttcc	960
cactcccgag	atgatactgg	ccggactgtc	gagaaatggg	agatcagaaa	ggcatataag	1020
ttcgggtggcg	accaagtaac	cttttcgcct	gatgagcaga	aggcgcttag	ggatttcggt	1080
gagccagtaa	tccgggttat	tgggttcaag	cctatcactg	cgcttccatt	ctgggcaaac	1140
gtcaagcacc	catatttat	ctatccatcc	gaggaagact	atgttaggctc	ctcgcgagta	1200
ttttccgcatt	tgcacatcagac	tctttgcgt	tccaagaaga	tggcactcgt	ctggttcatt	1260
gcacgcaagg	gtgctggccc	cgttctcgcc	gctatgatcg	caggcgaaga	aaagcttgat	1320
gagaatggcg	tacaaaaata	ccctcctggc	atgtggattc	ttcccctccc	cttcgcagac	1380
gatatccggc	agaacccga	aacaacgttg	aatgtcgccc	cggagtcatt	gattgatcag	1440
atgcgcgtga	tcgtccagca	actgcagctg	ccgaaggagg	tgtacgagcc	tctcaaatac	1500
cccaatccat	cccttcaatg	gcattaccgc	atcctacaag	ctctcgatt	agacgaagat	1560
ctccccgaaa	aaccagaaga	caaaaccatt	ccgaaatacc	gccaaatcga	caagcgcgcc	1620
ggtgactacg	tattatcctg	ggccgacgaa	ctcgaaaagc	aatacgccaa	aacctcagca	1680
gcggccccc	gcccaaccag	caccctcggt	aaacgaggat	caaaagacccg	agcaagcgaa	1740
accgaggact	ccaagccatc	aaaaaagatc	aaggttgagg	aagactctgg	aagcctagag	1800
gaggaagtcc	gcaggcatca	caagaaggga	acgctatcca	agcttacggt	cgctatccctc	1860
aaggacttct	tgacttccaa	tggacgctca	aatgccggta	agaaggcgga	tcttatttag	1920
cgggttagagg	agttcttggaa	gcagtga				1947

<210> 3
 <211> 648

<212> PRT

<213> Aspergillus niger

<400> 3

Met Ala Asp Gly Asn Pro His Arg Glu Asp Glu Ala Ala Glu Glu Glu
1 5 10 15

Glu Glu Ile Asp Glu Thr Ser Tyr Lys Pro Val Lys Asp Ala Val Leu
20 25 30

Phe Ala Ile Asp Val Ser Asp Ser Met Leu Thr Pro Arg Pro Ser Ala
35 40 45

Asp Pro Lys Lys His Thr Gln Glu Ser Pro Thr Thr Ala Ala Leu Lys
50 55 60

Cys Ala Tyr His Phe Met Gln Gln Arg Ile Ile Ser Asn Pro Gln Asp
65 70 75 80

Met Met Gly Val Leu Leu Phe Gly Thr Gln Ala Ser Lys Phe Phe Glu
85 90 95

Glu Asp Glu Asp Ser Arg Gly Asp Leu Ser Tyr Pro Asn Cys Tyr Leu
100 105 110

Phe Thr Asp Leu Asp Val Pro Ser Ala His Glu Val Lys Gly Leu Arg
115 120 125

Ala Leu Val Asp Asp Glu Gly Asp Ser Arg Glu Val Leu Ser Pro Ala
130 135 140

Lys Glu Gln Val Ser Met Ala Asn Val Leu Phe Cys Ala Asn Gln Ile
145 150 155 160

Phe Thr Ser Arg Ala Pro Asn Phe Leu Ser Arg Arg Leu Phe Ile Ile
165 170 175

Thr Asp Asn Asp Asn Pro His Gly Asp Asp Lys Thr Leu Arg Ser Ala
180 185 190

Ala Thr Val Arg Ala Lys Asp Leu Tyr Asp Leu Gly Val Thr Ile Glu
195 200 205

Leu Phe Pro Ile Ser Arg Pro Glu His Glu Phe Lys Asn Ser Lys Phe
210 215 220

Tyr Asp Ser Leu Pro Ser Asp Pro Glu Ala Pro Ala Tyr Leu Gln Ser
225 230 235 240

Asp Ser Lys Ala Ala Thr Ala Thr Gly Asp Gly Ile Ser Leu Leu Asn
245 250 255

Thr Leu Leu Ser Ser Ile Asn Ser Arg Thr Val Pro Arg Arg Thr His
260 265 270

Phe Ser Asn Met Pro Leu Glu Leu Gly Pro Asp Phe Arg Ile Ser Val
275 280 285

Ser Gly Tyr Ile Leu Leu Arg Arg Gln Ala Pro Ala Arg Asn Ser Phe
290 295 300

Ile Trp Leu Asn Gly Glu Lys Pro Val Val Ala Lys Gly Val Thr Ser
305 310 315 320

His Ser Ala Asp Asp Thr Gly Arg Thr Val Glu Lys Trp Glu Ile Arg
325 330 335

Lys Ala Tyr Lys Phe Gly Gly Asp Gln Val Thr Phe Ser Pro Asp Glu
340 345 350

Gln Lys Ala Leu Arg Asp Phe Gly Glu Pro Val Ile Arg Val Ile Gly
355 360 365

Phe Lys Pro Ile Thr Ala Leu Pro Phe Trp Ala Asn Val Lys His Pro
370 375 380

Tyr Phe Ile Tyr Pro Ser Glu Glu Asp Tyr Val Gly Ser Ser Arg Val
385 390 395 400

Phe Ser Ala Leu His Gln Thr Leu Leu Arg Ser Lys Lys Met Ala Leu
405 410 415

Val Trp Phe Ile Ala Arg Lys Gly Ala Gly Pro Val Leu Ala Ala Met
420 425 430

Ile Ala Gly Glu Glu Lys Leu Asp Glu Asn Gly Val Gln Lys Tyr Pro
435 440 445

Pro Gly Met Trp Ile Leu Pro Leu Pro Phe Ala Asp Asp Ile Arg Gln
450 455 460

Asn Pro Glu Thr Thr Leu Asn Val Ala Pro Glu Ser Leu Ile Asp Gln
465 470 475 480

Met Arg Val Ile Val Gln Gln Leu Gln Leu Pro Lys Gly Val Tyr Glu
485 490 495

Pro Leu Lys Tyr Pro Asn Pro Ser Leu Gln Trp His Tyr Arg Ile Leu
500 505 510

Gln Ala Leu Ala Leu Asp Glu Asp Leu Pro Glu Lys Pro Glu Asp Lys
515 520 525

Thr Ile Pro Lys Tyr Arg Gln Ile Asp Lys Arg Ala Gly Asp Tyr Val
530 535 540

Leu Ser Trp Ala Asp Glu Leu Glu Lys Gln Tyr Ala Lys Thr Ser Ala
545 550 555 560

Ala Ala Pro Arg Pro Thr Ser Thr Leu Val Lys Arg Gly Ser Lys Asp
565 570 575

Arg Ala Ser Glu Thr Glu Asp Ser Lys Pro Ser Lys Lys Ile Lys Val
580 585 590

Glu Glu Asp Ser Gly Ser Leu Glu Glu Glu Val Arg Arg His His Lys
595 600 605

Lys Gly Thr Leu Ser Lys Leu Thr Val Ala Ile Leu Lys Asp Phe Leu
610 615 620

Thr Ser Asn Gly Arg Ser Asn Ala Gly Lys Lys Ala Asp Leu Ile Glu
625 630 635 640

Arg Val Glu Glu Phe Leu Glu Gln
645

<210> 4

<211> 2651

<212> DNA

<213> Aspergillus niger

<400> 4

atggccgata aagaggcaac tgtctacatc gtggactgcg gcaagtccat	gggggagcgg	60
cgtcatggtc gcgaagtgac ggatctcgac tggcgatgc aatatgttg	ggatcgatt	120
acagggacgg tgagatcctt attcttgaga atcatatcat acatgaaagc	ttatgtttg	180
gataagggtgc cactggacga aaaatggctt tgatcggtgt tcttggctc	aggacagatg	240
gtgagtgact agcctccgg gtacagttgg tagttgtagt ttgctggtcg	gggctaattgc	300
aggaacgtcc agaaaccgct aatgagttgg aggatgatcc tgattattcg	cataatctcg	360
ttttgtctgg gattaaacag tatgattcat ttttgtctgc tgatcctctg	gttattcgct	420
gatgaactat aggtttctta tgccggatat ccggggtttgc agcgaccgaa	taaagcctag	480
caagactaat aaggagatg gtgagttact cttcttgtat ggaattggag	tgattgggc	540
tgagccgatg aatatacgta tctctgcact tggctcgcg attcagatga	ttatcactca	600
gtgcaagaaa ctgaagtaca agcgcaggat tgcctgggtt actaatggc	agggcccgat	660
gaacccggat aatcttagtg aaataacgaa gaagattaag gaggataaca	ttgaacttat	720
tattctgtta gtgtcaattt atacactgag agaaccgggg tactaacatg	ctgcagggg	780
ccagactttt atgatcctga atatgggtt aaagaggaag ataaagatcc	gcgaaaggta	840
tttaacttcg ttccatatgc tctagactaa taataacaat ggctacaggc	cgaaaatgaa	900
acactcctgc gtagtcttgc cgaagactgc gaaggagcct atggaaccct	agaacaagct	960
gttgcggagc tggaaactcc tcgtgtgaaa accacaagga taacagcaag	cttcaagggc	1020
cattgcaac taggaaaccc cgcaaatat gatactgcag ttcggatccc	tgtggagcgc	1080
tactacagga catacggtgc aaaagctccg tcggctagtc agttcacagt	acgtaacgaa	1140
gaggagatgg gaatggccgc ggccgcagcc ggctcgcagg aaggtagttc	ccttgggtt	1200
gttcgaaaca acaggtccta ccaaatttgc gatgggacta ctgaagaagg	ggtgaggagc	1260
gtggatcgag agcaacttgc caagggttat gactacgggc ggacattgtt	ccctatttagc	1320
gagacggatg agaatatcac cacccttagag acatttgcgg ctatcgagct	tcttgggtt	1380
atacagagcg atcgggttag ttctaccctc caataactgt tattatgtc	ctaagtgggt	1440
tttgcattt gtatgatcga tacatgcaca tgcgacgc aacatcatc	atcgccgcagc	1500
gcgcgaatga caaggcagca ctcgtcttt cctctttcat acatgcgcgt	tgcgactgg	1560
aatcgatgc tgcgtccgt atggtgctaa aggagaacaa accccctgtc	atagtcgtgc	1620
ttgcgcattt aatcgaaacc gactacgagt gtcgcctcg agcgcagg	ccattcgccag	1680
aagacgtacg aacgtaccgc ttccctccac tcgacagagt cattacagt	tctggtaaaag	1740
tggtgacaca gcatcgaaac ctacccaacg acgatctttt gatgcgatg	gacaaatacg	1800
tgaaaagcat ggagcttacc gatatggacg agaacgggtt agaagaattt	gaagtgtatct	1860
caacttcact gctgactttt tacaaagtga cccgacggaa tctctccaa	tagacgactc	1920
tttctctcca gtcctgcacc ggatcgactc cgcaatccgt caccgtgcc	ttcatccaa	1980
cgaccctatc ccgcggcccg cctcagtcct aacgaagttc tcccaccctc	cgatgaccc	2040
cgtcgagaag tccaagaaat acctagacaa gcttagtagca gtgtcgacg	tcaagaaagg	2100
tcagtccatc tcggccttga gcctcttagg ccccatcat actcacagt	atgaatctag	2160
tcccaccaaa aaccaaaggc accaaacgga cccgcgaaac cgagaagcca	ctatccggtc	2220

tcgacgtcga	tgcccttctc	caccaagaga	agcgcacgaa	gatctcaccc	aacaacgcaa	2280
ttcccgagtt	taagcagacg	ctctcgcagg	cagagaacat	cgagatcatc	aaggatgcag	2340
tgaagcagat	gagcactatc	attnaagacc	aaatcaggca	tagtcttgc	gatgttaatt	2400
atcatcggtt	cactgagggg	ctaggtgtga	tgcgggagga	actgatcgat	tatgaggaac	2460
ctgctctgt	taacgatttc	ttgaagcagc	tgaaggagaa	gttgttggaaa	gaggagctcg	2520
gtggggatcg	acgggagctg	tggtggctgc	taagaaggag	taagttgggg	ttgattgaac	2580
agagggagtc	ggaacactct	gaggtgagag	aagaggaagc	gaaggcgtt	atgtctatgg	2640
ctgctaagt	a					2651

<210> 5
 <211> 2178
 <212> DNA
 <213> *Aspergillus niger*

<400> 5						
atggccgata	aagaggcaac	tgtctacatc	gtggactgcg	gcaagtccat	gggggagcgg	60
cgtcatggtc	gcgaagtgac	ggatctcgac	tggcgatgc	aatatgttg	ggatcgatt	120
acagggacgg	tggccactgg	acgaaaaatg	gctttgatcg	gtgttcttg	gctcaggaca	180
gatgttgct	ggtcgggct	aatgcagggaa	cgtccagaaaa	ccgctaata	gttggaggat	240
gatcctgatt	attcgcatat	ctcggtttg	tctgggatta	aacagttct	tatgccggat	300
atccgggtt	tgagcgaccg	aataaagcct	agcaagacta	ataagggaga	tgctatctct	360
gcacttgc	tcgcgattca	gatgattatc	actcagtgc	agaaactgaa	gtacaagcgc	420
aggattgtcc	tggttactaa	tggcagggc	ccgatgaacc	cgataatct	tagtgaata	480
acgaagaaga	ttaaggagga	taacattgaa	cttattattc	tgggaccaga	ctttgatgat	540
cctgaatatg	gggtgaaaga	ggaagataaa	gatccgcga	aggccaaaa	tgaaacactc	600
ctgcgtagtc	ttgccgaaga	ctgcgaagga	gcctatggaa	ccctagaaca	agctgttgcg	660
gagctggaaa	ctcctcggt	gaaaaccaca	aggataacag	caagcttcaa	ggccatttg	720
caactaggaa	accccgcaga	atatgatact	gcagttcgga	tccctgtgga	gctactac	780
aggacatacg	ttgcaaaagc	tccgtcggt	agtcagttca	cagtacgtaa	cgaagaggag	840
atggaaatgg	ccgcggccgc	agccggctcg	caggaaggta	gttccctgt	gggtgttcga	900
aacaacaggt	cctaccaa	tgacgatggg	actactgaag	aagggtgag	ggacgtggat	960
cgagagcaac	ttgccaaggg	ttatgagtac	ggcggacat	tggccctat	tagcgagacg	1020
gatgagaata	tcaccaccct	agagacattt	gcccgtatcg	agttcttgg	gtttatacag	1080
agcgatcggt	atgatcgata	catgcacatg	tcgacgacaa	acatcatcat	cgcgacgc	1140
gcgaatgaca	aggcagcact	cgctcttcc	tcttcatac	atgcgtgtt	cgagctggaa	1200
tcgtacgctg	tcgcccgtat	ggtgctaaag	gagaacaaac	cccctgtcat	agtcgtgtt	1260
gcccacatcaa	tcgaacccga	ctacgagtgt	ctccctcgaag	cgcagttgcc	attcgcagaa	1320
gacgtacgaa	cgtaccgctt	ccctccactc	gacagagtca	ttacagtgtc	tggtaaagt	1380
gtgacacagc	atcgaaaccc	accaacgac	gatctgttga	atgcgtatgg	caaatacgt	1440
aaaagcatgg	agcttaccga	tatggacgag	aacggtgacc	cgacggatc	tctcccaata	1500
gacgactctt	tctctccagt	cctgcaccgg	atcgactccg	caatccgtca	ccgtgccatt	1560
catcccaacg	accctatccc	gcccccagcc	tcagtcctaa	cgaagttctc	ccaccctccg	1620
gatgacctcg	tcgagaagtc	caagaaatac	ctagacaagc	tagtagcagt	gtcgacgtc	1680
aagaaaagtcc	caccaaaaac	caaaggcacc	aaacggaccc	cgaaaaccga	gaagccacta	1740
tccggtctcg	acgtcgatgc	ccttctccac	caagagaagc	gcacgaagat	ctcaccacaa	1800
aacgcaattc	ccgagtttaa	gcagacgctc	tcgcaggcag	agaacatcga	gatcatcaag	1860
gatgcagtga	agcagatgag	cactatcatt	gaagacaaa	tcaggcatag	tcttggcgat	1920
gttaattatc	atcggttcac	tgaggggcta	ggtgtgtatgc	gggaggaact	gatcgattat	1980
gaggaacctg	ctctgtataa	cgatttcttg	aagcagctga	aggagaagtt	gttggaaagag	2040
gagctcggtg	gggatcgacg	ggagctgtgg	tggctgctaa	gaaggagtaa	gttggggttg	2100
attgaacaga	gggatcgacg	acactctgag	gtgagagaag	aggaagcgaa	ggcgatcgat	2160
tctatggctg	ctaagt	ga				2178

<210> 6
 <211> 725

<212> PRT

<213> Aspergillus niger

<400> 6

Met Ala Asp Lys Glu Ala Thr Val Tyr Ile Val Asp Cys Gly Lys Ser
1 5 10 15

Met Gly Glu Arg Arg His Gly Arg Glu Val Thr Asp Leu Asp Trp Ala
20 25 30

Met Gln Tyr Val Trp Asp Arg Ile Thr Gly Thr Val Ala Thr Gly Arg
35 40 45

Lys Met Ala Leu Ile Gly Val Leu Gly Leu Arg Thr Asp Val Cys Trp
50 55 60

Ser Gly Leu Met Gln Glu Arg Pro Glu Thr Ala Asn Glu Leu Glu Asp
65 70 75 80

Asp Pro Asp Tyr Ser His Ile Ser Val Leu Ser Gly Ile Lys Gln Phe
85 90 95

Leu Met Pro Asp Ile Arg Gly Leu Ser Asp Arg Ile Lys Pro Ser Lys
100 105 110

Thr Asn Lys Gly Asp Ala Ile Ser Ala Leu Val Leu Ala Ile Gln Met
115 120 125

Ile Ile Thr Gln Cys Lys Lys Leu Lys Tyr Lys Arg Arg Ile Val Leu
130 135 140

Val Thr Asn Gly Gln Gly Pro Met Asn Pro Asp Asn Leu Ser Glu Ile
145 150 155 160

Thr Lys Lys Ile Lys Glu Asp Asn Ile Glu Leu Ile Ile Leu Gly Pro
165 170 175

Asp Phe Asp Asp Pro Glu Tyr Gly Val Lys Glu Glu Asp Lys Asp Pro
180 185 190

Arg Lys Ala Glu Asn Glu Thr Leu Leu Arg Ser Leu Ala Glu Asp Cys
195 200 205

Glu Gly Ala Tyr Gly Thr Leu Glu Gln Ala Val Ala Glu Leu Glu Thr
210 215 220

Pro Arg Val Lys Thr Thr Arg Ile Thr Ala Ser Phe Lys Gly His Leu
225 230 235 240

Gln Leu Gly Asn Pro Ala Glu Tyr Asp Thr Ala Val Arg Ile Pro Val
245 250 255

Glu Arg Tyr Tyr Arg Thr Tyr Val Ala Lys Ala Pro Ser Ala Ser Gln
260 265 270

Phe Thr Val Arg Asn Glu Glu Met Gly Met Ala Ala Ala Ala Ala
275 280 285

Gly Ser Gln Glu Gly Ser Ser Leu Val Gly Val Arg Asn Asn Arg Ser
 290 295 300
 Tyr Gln Ile Asp Asp Gly Thr Thr Glu Glu Gly Val Arg Asp Val Asp
 305 310 315 320
 Arg Glu Gln Leu Ala Lys Gly Tyr Glu Tyr Gly Arg Thr Leu Val Pro
 325 330 335
 Ile Ser Glu Thr Asp Glu Asn Ile Thr Thr Leu Glu Thr Phe Ala Ala
 340 345 350
 Ile Glu Leu Leu Gly Phe Ile Gln Ser Asp Arg Tyr Asp Arg Tyr Met
 355 360 365
 His Met Ser Thr Thr Asn Ile Ile Ile Ala Gln Arg Ala Asn Asp Lys
 370 375 380
 Ala Ala Leu Ala Leu Ser Ser Phe Ile His Ala Leu Phe Glu Leu Glu
 385 390 395 400
 Ser Tyr Ala Val Ala Arg Met Val Leu Lys Glu Asn Lys Pro Pro Val
 405 410 415
 Ile Val Val Leu Ala Pro Ser Ile Glu Pro Asp Tyr Glu Cys Leu Leu
 420 425 430
 Glu Ala Gln Leu Pro Phe Ala Glu Asp Val Arg Thr Tyr Arg Phe Pro
 435 440 445
 Pro Leu Asp Arg Val Ile Thr Val Ser Gly Lys Val Val Thr Gln His
 450 455 460
 Arg Asn Leu Pro Asn Asp Asp Leu Leu Asn Ala Met Asp Lys Tyr Val
 465 470 475 480
 Lys Ser Met Glu Leu Thr Asp Met Asp Glu Asn Gly Asp Pro Thr Glu
 485 490 495
 Ser Leu Pro Ile Asp Asp Ser Phe Ser Pro Val Leu His Arg Ile Asp
 500 505 510
 Ser Ala Ile Arg His Arg Ala Ile His Pro Asn Asp Pro Ile Pro Pro
 515 520 525
 Pro Ala Ser Val Leu Thr Lys Phe Ser His Pro Pro Asp Asp Leu Val
 530 535 540
 Glu Lys Ser Lys Lys Tyr Leu Asp Lys Leu Val Ala Val Ser Asp Val
 545 550 555 560
 Lys Lys Val Pro Pro Lys Thr Lys Gly Thr Lys Arg Thr Arg Glu Thr
 565 570 575
 Glu Lys Pro Leu Ser Gly Leu Asp Val Asp Ala Leu Leu His Gln Glu
 580 585 590

Lys Arg Thr Lys Ile Ser Pro Asn Asn Ala Ile Pro Glu Phe Lys Gln
595 600 605

Thr Leu Ser Gln Ala Glu Asn Ile Glu Ile Ile Lys Asp Ala Val Lys
610 615 620

Gln Met Ser Thr Ile Ile Glu Asp Gln Ile Arg His Ser Leu Gly Asp
625 630 635 640

Val Asn Tyr His Arg Val Thr Glu Gly Leu Gly Val Met Arg Glu Glu
645 650 655

Leu Ile Asp Tyr Glu Glu Pro Ala Leu Tyr Asn Asp Phe Leu Lys Gln
660 665 670

Leu Lys Glu Lys Leu Leu Lys Glu Glu Leu Gly Gly Asp Arg Arg Glu
675 680 685

Leu Trp Trp Leu Leu Arg Arg Ser Lys Leu Gly Leu Ile Glu Gln Arg
690 695 700

Glu Ser Glu His Ser Glu Val Arg Glu Glu Glu Ala Lys Ala Phe Met
705 710 715 720

Ser Met Ala Ala Lys
725

<210> 7

<211> 4501

<212> DNA

<213> Aspergillus niger

<400> 7

cagctcattc agagagctac ccgttaga acaggaatac tggggattt gtgagaacgc 60
gaccgcacga ccgccttcc cattccaaa gccatcttcc agcaattgtg tgtacatttgc 120
ttccgtcagc gggttggcgt aacggaaggc aacgtacggc ttgtgaggcg cagtctccgg 180
gttgcatttgc tccagcagct tgcacatttc cttgcattgg tattccgacc attttcttat 240
gggtgagcct ccgcgcgtgt ccgcatactg ctttgaatc ttgggtgtgc gtcgtttcga 300
aataagagggc ccgaggtaat gctggactt gccaagaggg atcaaatcgc cgtcggcctt 360
aatatagaatg agaatgttag aaacgttaga accagaatga cagcttgcctt tagtcggaga 420
cgtacaaaga gccggctgag gaaatcctt acttcgtctg tcgtcgaggcc cctcccatg 480
ttcaggaaga ccatggctgtt agggccctta gagcctgttgc catcctgggt aaccggaggc 540
actgttgttgc ccagcccaca tctttgttct tgcttgcatac cgaacagggt gcgagaagcc 600
ggtcgcagca attgccgggg cagggtaaac gggcggcgga gagccatgac aggttaattgt 660
actgaattcg gttgacctag tcaatggagg taataagaaa agaccgttcg tatcgccaa 720
gcagatgaac tattcacgccc gcattaaata ttcaaaagat ggacgagtgg caagaacagg 780
tagtgggtgt atacaacagc gcaaggcctt ctggaaagctg aaaagtccag aacggcttgc 840
tgacggagca ccgagaccac gaccaactcc gactcccgc acgcaatgac cggccagcta 900
gcgtcatcaa ttaccggcg gacatcacat gatgttcgttgc tctcccccgc tctttctgccc 960
caccggtttgc atcgcgtccc tcgcgcacgg atccagtgc gatatacgat gatctatctc 1020
cggtgcagg cagcagaggc caaacaggca gacacaacag ccccaacttgc tcctgggttac 1080
gattcaagtt gtcttaacctt tataacttcc ctctttcaat ttgcataata tcttgaatgc 1140
tttaaacat tccacaacat tctactatgg cggacggcaa cccacatcgga gaagatgagg 1200
cggccgagga agaagaggag attgatgaga ctgtacgcaa atttacccat gaacttggac 1260
tggaaactctg gaactgacaa taagatcaga gctacaaacc agtcaaagat gcggcctct 1320

tcgcaatcga	tgtcagcgat	tccatgttga	cgccctcgccc	ctcagcagat	cctaagaaac	1380
acacccaaga	atcacccacc	acggcagcgc	tcaaatgcgc	ctatcacttc	atgcaacaac	1440
gaatcatatc	aaatccacaa	gacatgatgg	gtgtttgct	gttcgggacc	caggcgtcca	1500
agttcttga	agaagatgaa	gacagtcggg	gagacctgtc	ctaccccaac	tgctacatct	1560
tcactgatct	ggatgttcct	tcggctcatg	aggtaaagg	acttcgagca	ctggtagatg	1620
atgaaggaga	ctcaagggag	gttctatctc	cagcgaaaga	gcaggtctct	atggcaaacg	1680
tcctatTTG	cgccaaccag	atattcacat	ccagagcgcc	aaatttctc	tcccggcggt	1740
tgttcatcat	aaccgacaat	gacaaccccc	atggtgatga	taaaaccctg	cggtcagcgg	1800
cgactgtacg	tgctaaggat	cttacgatc	ttgggtgtcac	aattgagctg	tttccgatct	1860
cacGCCCTGA	gcatgagttc	aagaacagca	agttctatga	cgtaagctat	catactctat	1920
agcaaagtgg	caggggtcga	tactcactac	agatacaaag	gatattatct	acaagtctt	1980
gcccagcgat	ccagaggcgc	ctgcataatct	acaatctgtat	tcaaaagcgg	cgactgcgac	2040
cggggacggg	atttcactcc	tcaacacgct	tctgtccagt	attaattcga	gaacgggtcc	2100
gcgtcgcact	cattttcga	acatgcctt	agaacttggc	ccagacttca	gaatttcggt	2160
atcgggctat	atactcttac	gaaggcaagc	gcccgtaga	aactccttca	tctggctgaa	2220
cggcgagaag	cctgtggtcg	cgaaaggagt	gacttcccac	tccgcagatg	atactggccg	2280
gactgtcgag	aaatgggaga	tcagaaaggc	atataagttc	ggtggcgacc	aagtaacctt	2340
ttcgcctgat	gagcagaagg	cgcttaggga	tttcggtgag	ccagtaatcc	gggttattgg	2400
gttcaagcct	atcactgcgc	ttccattctg	ggcaaacgtc	aagcaccat	attttatcta	2460
tccatccgag	gaagactatg	taggctcctc	gcgagtattt	tccgcattgc	atcagactct	2520
tttgcgttcc	aagaagatgg	cactcgtctg	gttcattgca	cgcaagggtg	ctggccccgt	2580
tctcggcgct	atgatcgca	gcgaagaaaaa	gcttgatgag	aatggcgatc	aaaaataaccc	2640
tcctggcatg	tggattcttc	ccctccccc	cgcagacgtat	atccggcaga	accccgaaac	2700
aacgttgaat	gtcgccccgg	agtcattgtat	tgatcagatg	cgcgtatcg	tccagcaact	2760
gcagctgccc	aaggaggtgt	acgagcctct	caaatacccc	aatccatgtat	agtcacttct	2820
gtcttgcatt	gctcgtatac	gatgaacgag	aagctgacag	cccgtatca	gcccttcaat	2880
ggcattaccg	catcctacaa	gctctcgcat	tagacgaaga	tctcccgaa	aaaccagaag	2940
acaAAAACCAT	tccgaaatac	cgccaaatcg	acaaggtaaa	tccaccacac	ccaacacgag	3000
aaataaccct	ccaggcgtcc	aacttactga	caattgcacc	acagcgcgcc	ggtgactacg	3060
tattatcctg	ggccgacgaa	ctcgaaaagc	aatacgccaa	aacctcagca	gccccccctc	3120
gccccaccag	caccctcggt	aaacgaggat	caaaagaccg	agcaagcgaa	accgaggact	3180
ccaagccatc	gaaaaagatc	aaggttgagg	aagactctgg	aagcttagag	gaggaagtcc	3240
gcagggcatca	caagaaggga	acgctatcca	aggtaagcca	ccacaggctt	tctacacgtc	3300
ctcgtatgg	caaataatgac	atcgtattaa	ccggcggtt	tctagcttac	gttcgtatc	3360
ctcaaggact	tcttgacttc	caatggacgc	tcaaatacgcc	gtaagaaggc	ggatcttatt	3420
gagcgggtag	aggagttctt	ggagcagtga	catggcgaaa	ttgttggatt	cgctagtgcg	3480
cttctgttgg	tggatgtcg	tatgtgggt	cttatctcg	gtttaggcgtt	cgtgacactga	3540
ggacatgagc	ttgtaattaa	tgtgggttg	gatgtcgccg	tattcgatct	tcagcgaaac	3600
gtaatggaca	cgtatTTT	gcatgttaca	gttataaaaa	atcgaattcg	ctgggcttagc	3660
cggacatgtc	aaaacgaaga	gcattaggag	agacatatca	ggtccaagtg	ctatcttca	3720
aaccagtgc	ttaagatcac	cgaggcattt	atctccagaa	aattcaccgg	ttcagcaggt	3780
gcfgtatcc	cgaattcaaa	ttaatattgg	aacgatcgta	aataaccacc	cagattcgcc	3840
gtaaacgata	gtagtcaggc	tttgcgcgg	acagaagggg	acgagtatgt	caactgagtc	3900
aacttgaacc	gagcagtccc	tgtaaacaac	gccacgctgt	ttgtatatac	ccttttagaaa	3960
cgtattgtcg	ctggcaatta	tccacaaaaaa	atgagtctaa	acggggcgaaa	aaagtccaccc	4020
gaatgggaga	atatgtggaa	agaagaaaga	aagagagacc	aaagcaagag	agcgccgaaa	4080
ggaagctatc	gtaatata	caagtagaa	ccgtgggtat	ttttataaaa	agcagaaacg	4140
ttaacggat	gcgtacaatg	atcaacatgg	tccataaaact	tgacagtagc	agacttcttc	4200
gtcgggacag	ctgagagtag	caaagtgtt	gtatTTT	cgcatc	aggttaggggg	4260
ggaggggtgc	aaaggcaaca	tactatattg	attcttgc	aatatgaca	tgccagagaa	4320
attccatgac	acggccacta	ctggcgtcat	ccttgcgtgt	atcgattatc	cactggcgga	4380
tcttgcgtat	gtcctctcg	ggtcgtcggt	ggacctgctc	ccgggacacg	gcaattgcg	4440
cacagcacgc	cgcgccaatc	tgtttcgga	tttgcaggaa	cttctggat	ttagcttcgt	4500
c						4501

<211> 4702
 <212> DNA
 <213> Aspergillus niger

<400> 8

cactcaggat	tcttatatct	tatggggccc	aagtatctct	gcagtcaggc	gaccaaggaa	60
cagcgttgca	cgctgctgtg	gtgggtggct	ttcacggctc	agtcaatttg	cttctgacag	120
aaaatgcgga	ggttgatgca	tcatgtacac	tcattggac	cccgttggcg	gcagtcatgc	180
ctcgtaaatg	gaagtcctgc	tgtggtcgtt	accatcgaag	ctgtgctgag	caattaattg	240
cttggggtgc	agatattgat	cgcattgatg	aacgtctggg	gactccaatg	gacattgcat	300
acaaggcagg	aaacaatgag	ggtgtggagc	tgttacttga	gaatggagca	ctggatccca	360
aatccacagc	gtatccacta	aattcggaca	attgaccggg	cacgaagtgc	ttttctgttt	420
gagatata	tggagcactg	aagaaaataa	tcagagactt	gccgtactt	aaaacttgg	480
gaaatgatcg	gatcgtaaa	tgtccaattt	gccctgggt	tctgggctcg	caagaccct	540
ttaaaaataat	atagacattc	acgcactact	cgcagcaa	cttaacaatt	tgggcttgc	600
taagctctgg	gagatacta	atttattata	gaaccttcaa	atgtcgatta	gtatgtgaga	660
gttatcttgc	caattcagcc	tgttagtaca	ataaaaaccc	ctcatagcgg	ctccgtcata	720
tataaaattt	tgcactacac	tcacttgcga	tatatgatgc	gcagacaccc	atgttagtat	780
ctgcaatgtc	acttcaattt	cgccaaacaaa	ggaccctcca	taaagttagt	actctgcaat	840
ttaaatact	agacttgtat	cacaatcat	gtaaataaaag	caatacggag	tataagctgc	900
ccactgcatg	cccctcttag	taagcaccca	ctgcatgatg	tcatgtgctt	tcgcgtcccg	960
cccgctccca	atcgggaaat	atcacgcgtc	tgcctactca	gagtgcattt	ttctgccttg	1020
agctcgtccc	ttttatgtcg	agccagctgc	ggcatcgaat	ggatctgatt	ccatcgataa	1080
tctcagtcat	tcatactgaa	aatggccat	aaagaggcaa	ctgtctacat	cgtggactgc	1140
ggcaagtcca	tgggggagcg	gcgtcatggt	cgcgaagtga	cggatctcga	ctgggcatg	1200
caatatgtt	gggatcgtat	tacagggacg	gtgagatcct	tattctttag	aatcatatca	1260
tacatgaaag	ctttagttt	ggataggtgg	ccactggacg	aaaaatggct	ttgatcggt	1320
ttcttgggct	caggacagat	ggtgagtgac	tagcctcccg	ggtacagtt	gtagttgt	1380
tttgctggtc	ggggctaattg	caggaacgtc	cagaaaccgc	taatgagtt	gaggatgatc	1440
ctgattattc	gcatatctcg	gttttgcctg	ggattaaaca	gtatgattca	tttttgcctg	1500
ctgatcctct	ggttattcgc	tgtgaacta	tagtttctt	atgccggata	tccggggtt	1560
gagcgaccga	ataaaagccta	gcaagactaa	taagggagat	ggtgagttac	tcttcttgta	1620
tggaatttgg	gtgattgggg	ctgagccat	gaatatacg	atctctgcac	ttgtgcgc	1680
gattcagatg	attatcactc	agtcaagaa	actgaagtgac	aagcgcagga	ttgtcctgt	1740
tactaatggg	cagggcccga	tgaacccga	taatcttagt	gaaataacga	agaagattaa	1800
ggaggataac	attgaactt	ttattcttt	agtgtcaatt	gatacactga	gagaaccggg	1860
gtactaacat	gctgcagggg	accagactt	gatgatcctg	aatatggggt	gaaagaggaa	1920
gataaagatc	cgcgaaaggt	atthaacttc	gtccatatg	ctctagacta	ataataacaa	1980
tggctacagg	ccgaaaatga	aacactcctg	cgtgtctt	ccgaagactg	cgaaggagcc	2040
tatggaaccc	tagaacaagc	tgttgcggag	ctggaaactc	ctcgtgtgaa	aaccacaagg	2100
ataacagcaa	gcttcaaggg	ccatttgc当地	ctaggaaacc	ccgcagaata	tgatactgca	2160
gttcggatcc	ctgtggagcg	ctactacagg	acatacggt	caaaagctcc	gtcggctag	2220
cagttcacag	tacgtacga	agaggagat	ggaatggccg	cggccgcagc	cggctcgcag	2280
gaaggtagtt	cccttgc当地	tgttgc当地	aacaggtctt	accaaattga	cgatggact	2340
actgaagaag	gggtgaggga	cgtggatcga	gagcaactt	ccaagggtt	tgagtgacgg	2400
cgacattgg	tcccttattag	cgagacggat	gagaatatca	ccaccctt当地	gacatttgc当地	2460
gctatcgagc	ttcttggggtt	tatacagagc	gatcgggt	gttctaccct	ccaataactg	2520
ttattatgct	gctaagtggg	ttttgc当地	agtatgatc	atcatgc当地	atgtcgacg	2580
caaacatcat	catcgccag	cgcgc当地	acaaggcagc	actcgctt	tcctctt当地	2640
tacatgc当地	gttcgagct	gaatcgatc	ctgtcgcc	tatggt	aaggagaaca	2700
aacccctgt	catagtcgt	cttgc当地	caatcgaacc	cgactacg	tgtctc当地	2760
aagcgcagtt	gccattcgca	gaagacgtac	gaacgtacc	cttccctt当地	ctcgacagag	2820
tcattacagt	gtctggtaaa	gtgggtacac	agcatcgaaa	cctacccaa	gacgatctgt	2880
tgaatgc当地	ggacaaatac	gtgaaaagca	tggagtt	cgatatgg	gagaacggg	2940
gagaagaatt	ggaagtgatc	tcaactt	tgctgactt	gtacaaatg	acccgacgg	3000
atctcttcca	atagacgact	ctttctctcc	agtcc	cgatcgact	ccgcaatccg	3060
tcaccgtgcc	attcatccca	acgaccctat	cccgc当地	gcctcag	taacgaagtt	3120

ctcccaccct	ccggatgacc	tcgtcgagaa	gtccaagaaa	tacctagaca	agcttagtagc	3180
agtgtcggac	gtcaagaaaag	gtcagtccat	ctcggccttg	agcctcttag	gcccccatca	3240
tactcacagt	gatgaatcta	gtcccaccaa	aaaccaaagg	caccaaacgg	acccgcgaaa	3300
ccgagaagcc	actatccggt	ctcgacgtcg	atgcccttct	ccaccaagag	aagcgcacga	3360
agatctcacc	caacaacgca	attcccaggt	ttaaggcagac	gctctcgac	gcagagaaca	3420
tcgagatcat	caaggatgca	gtgaaggcaga	tgagcactat	cattgaagac	caaatcaggc	3480
atagtcttgg	cgatgttaat	tatcatcggt	tcactgaggg	gctaggtgtg	atgcgggagg	3540
aactgatcga	ttatgaggaa	cctgctctgt	ataacgattt	cttgaagcag	ctgaaggaga	3600
agttgtgaa	agaggagctc	ggtggggatc	gacgggagct	gtgggtggctg	ctaagaagga	3660
gtaagttggg	gttgattgaa	cagagggagt	cggaacactc	tgaggtgaga	gaagaggaag	3720
cgaaggcggt	tatgtctatg	gctgctaagt	gagcagaccg	ttattgtatcc	ctattgtcc	3780
ccgattaagg	actgggcaac	agttcgataa	tgacaaatga	acaagctcca	atgctgcatt	3840
actgtgctcg	ctagagtaca	atattcacga	taaccctcg	ctaagtaaca	aggcttatcc	3900
catgccaat	gtaacacaca	taacatataa	taccaaattc	gatgaacagt	acacggata	3960
tcaatcatga	ccatgagtag	aaatagacat	cgcaagcaac	cattatatcc	acacactcaa	4020
gaaattctcc	caatccttt	cttccaata	tcaatcttcc	cacccaaacct	atattcaagt	4080
cagcacaact	ttaccatcaa	aaagtaagaa	caagatggg	aaaaagaaca	tacctcgtag	4140
catcctcatc	cgccaaattc	aacaactcat	tctgcaccc	caactcattt	ttaattgca	4200
tccccaactc	cttctgccga	ttgacaatcc	tcatcaactc	atccaccgcg	acatcctgat	4260
cctccatcat	ctgcttctgc	aactgcacca	ccccactatt	atccaactcg	cgcgtcctct	4320
ccgtctccct	ccccaaacact	ctccccgacg	accgaatcgc	cttcttgccc	ccctgcgtcc	4380
ccatcaacgc	ctccttatcc	tgaatcgacg	ccaccgcact	atcaatccga	ctcttcgccc	4440
ccatcgatt	caacagatcc	tccagtccat	ctttctccct	cctcgcgttg	atgagtagat	4500
ccttccgtcg	tcgcatctct	ccttccccga	gcgtgttgg	cccactaaca	ctccatgccc	4560
tggcggtcg	agctgttattt	ctgcgcccga	gtttacttcc	tggctttgac	cctgcattat	4620
tttcctcccc	acctccagaa	gaagagttac	tcaaattcct	caacccactc	tccaaactcg	4680
caatcaatcc	cccgccctta	ac				4702

<210> 9
 <211> 3965
 <212> DNA
 <213> Aspergillus niger

<400> 9						
gtttgacgcg	tttgcagtgt	agaagcttcc	agctaccgta	gattactgat	acaaactcaa	60
tacactattt	ctataacctt	actgttcaat	acagtacgt	caaaatttcc	ggaatattaa	120
tgttacgggt	accttccata	tgttagactag	cgcaacttggc	attagggttc	gaaatacgat	180
caaagagtat	tgggggggggt	gacagcagta	atgactccaa	ctgtaaatcg	gcttcttaggc	240
gcgctccatc	taaatgttct	ggctgtggtg	tacagggca	taaaattacg	cactaccga	300
atcgatagaa	ctactcattt	ttatatagaa	gtcagaattc	atgggtttt	gatcatttta	360
aattttata	tggcggtgg	tggcaactc	gcttgcgcgg	gcaactcgct	taccgattac	420
gttagggctg	atatttacgt	aaaaatcgct	aagggtatgc	agaccaaagt	actaaaaccc	480
cgaggtaac	agcatccaag	cccaagtcc	tacggagaa	accccagcgt	ccacatcag	540
agcgaaggac	caccccttagg	catcgacgc	accatccaa	tagaaggcagc	aaagcgaaac	600
agcccaagaa	aaaggtcgcc	ccgtcgccct	tttctgcaac	gctgatcacg	ggcagcgatc	660
caaccaacac	cctccagagt	gactaggggc	ggaaatttat	cgggattaat	ttccactcaa	720
ccacaaatca	cagtcgtccc	cggatttgc	ctgcagaatg	caatttaaac	tcttctgcga	780
atcgcttgg	ttccccgccc	ctggccgtag	agcttaaagt	atgtcccttg	tcgatgcgt	840
gtatcacaac	atataaatac	tagcaaggg	tgccatgctt	ggaggatagc	aaccgacaac	900
atcacatcaa	gctctccctt	ctctgaacaa	taaaccac	agaaggcatt	tatgatggtc	960
gcgtgggtgg	ctcttatttct	gtacggccctt	caggtcgccg	cacctgcttt	ggctgcaacg	1020
cctgcggact	ggcgatcgca	atccatttat	ttccttctca	cggatcgatt	tgcaaggacg	1080
gatgggtcga	cgactgcgac	ttgtataact	gcccgtcagg	tgtgttggta	cctactagct	1140
ttcagaaaga	ggaatgtaaa	ctgacttgc	atagaaatac	tgtggtgaa	catggcaggg	1200
catcatcgac	aaggtaaatt	gccctttat	caaaaaaaaaa	agaaggaaaa	gcagaagaaa	1260
aataaaataa	aaagaactct	agtccaaacc	atcacatagt	tggactatat	ccagggaaatg	1320

ggcttcacag	ccatctggat	caccccccgtt	acagccccagc	tgccccagac	caccgcata	1380
ggagatgcct	accatggcta	ctggcagcag	gatatgtaag	tcgatttctt	taaatatcta	1440
cctgtcatct	tttacatcaa	tatgaactaa	cttgatggtt	ttagatactc	tctgaacgaa	1500
aactacggca	ctgcagatga	cttgaaggcg	ctctcttcgg	cccttcatga	gagggggatg	1560
tatcttatgg	tcgatgttgt	tgctaaccat	atggttcgtg	gtccttgca	actgacttcg	1620
cggatatggt	tcatttcagt	actgacaatg	agtaatatca	gggctatgat	ggagcgggta	1680
gctcagtcga	ttacagtgtg	tttaaaccgt	tcagttccca	agactactc	caccggttct	1740
gtttcattca	aaactatgaa	gatcagactc	agttgagga	ttgctggta	ggagataaca	1800
ctgtctcctt	gcctgatctc	gataccacca	aggatgttgt	caagaatgaa	tggtacgact	1860
gggtgggatc	attggtatcg	aactactcca	gtaagatatt	tctccctcat	tctacaactt	1920
ggctgatcga	tgatacttac	gaaatcagg	gacggcctcc	gtatcgacac	agtaaaacac	1980
gtccagaagg	acttctggcc	cgggtacaac	aaagccgcag	gcgtgtactg	tatcggcgag	2040
gtgctcgacg	gtgatccggc	ctacacttg	ccctaccaga	acgtcatgga	cgccgtactg	2100
aactatccca	tgtatggttc	ctccaaccat	gagccttctt	gcaagtctca	tctcctaactg	2160
aaacggctaa	aaccagttac	tatccactcc	tcaacgcctt	caagtcaacc	tccggcagca	2220
tggacgacct	ctacaacatg	atcaacacccg	tcaaattcga	ctgtccagac	tcaacactcc	2280
tggcacatt	cgtcgagaac	cacgacaacc	cacggttcgc	ttcgttaagtc	ttccctttta	2340
ttttccgttc	ccaatttcca	cacagaaccc	cacctaacaa	gagcaaagtt	acaccaacga	2400
catagccctc	gccaaagaacg	tcgcagcatt	catcatcctc	aacgacggaa	tccccatcat	2460
ctacgcccggc	caagaacagc	actacgcccgg	cgaaaacgac	cccgcgaacc	gcgaagcaac	2520
ctggctctcg	ggctacccg	ccgacagcga	gctgtacaag	ttaattgcct	ccgcgaacgc	2580
aatccggaac	tatgccatta	gcaaagatac	aggattcgtg	acctacaagg	taagcacaac	2640
ctctaagcat	accctaattgg	cctatcttca	gagtatctga	cacaagagac	taatcactgg	2700
caatacagaa	ctggcccattc	tacaaagacg	acacaacgat	cgccatgcgc	aagggcacag	2760
atgggtcgca	gatcgtgact	atcttgc	acaagggtgc	ttcgggtgat	tcgtataaccc	2820
tctcctttag	tggtgcgggt	tacacagccg	gccagcaatt	gacggaggtc	attggctgca	2880
cgaccgtgac	ggttggttcg	gatggaaatg	tgccctgttcc	tatggcaggt	gggctaccta	2940
gggtatttta	tccgactgag	aagttggcag	gtagcaagat	ctgttagtagc	tcgtgaaggg	3000
tggagagtt	atgatggtac	tgcttattcaa	tctggcattt	gacagttagt	ttgagtttga	3060
tgtacataac	caaggttgtg	tctgtataat	atatacatgt	aagatacatg	agcttcggtg	3120
atataataca	gaagtaccat	acagtaccgc	gttatgaaaa	cacattaatc	cgatccctt	3180
cctataatag	actagcgtgc	ttggcattag	ggttcgaaaa	acaatcgaag	agtataaggg	3240
gatgacagca	gtaacgactc	caactgttagc	ccacatcttgc	agttcggcaa	ctactgttgg	3300
cacgtgaccc	tgtgccttgc	ggtagctcct	taactttgtc	atcattcgaa	gaattttcg	3360
cccttcccag	gtaccatcca	aaagacaagc	atccgtcgct	tcactctgag	atcagatgag	3420
agtaatattt	ttgactgcgt	ttgtgatgcg	ggtgatgtcc	tctgcgatcg	gccgcaagct	3480
gtttagtttgc	ccccggatct	tctgtgcccga	cggttgctcc	ccgaattttc	ttagctagtg	3540
taatcacgct	attcagaaag	gcttccaaga	attaggccgg	tagttcggcg	cgtttgggtgt	3600
cgtcaagctc	cagcagtgc	ggggcctcgg	ctatgatatg	gttagaatgc	tcgggggtgg	3660
tcacggcagg	acacccgaca	ctgcaacgtc	taccacattt	gagcgttatt	ggcagacttg	3720
cggcgagata	acgaccgcta	gcttgtatca	accaaattcca	actgaaatta	ttgcttgc	3780
atcccaacag	tggatttcgg	aggagggagg	gggaaagata	tacgatgaac	ggaagactgg	3840
acaagatacg	ttacataaaag	cagtaact	tgtttcaa	tgtgtacaca	ccagggctct	3900
cgcttcagcg	gagagtgtcg	aaagattcag	taaaacatcg	ccaggggtga	tggaaagggg	3960
ttaag						3965

<210> 10
 <211> 1497
 <212> DNA
 <213> Aspergillus niger

<220>
 <221> CDS
 <222> (1)..(1497)

<400> 10

atg gtc gcg tgg tgg tct cta ttt ctg tac ggc ctt cag gtc gcg gca Met Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala 1 5 10 15	48
cct gct ttg gct gca acg cct gcg gac tgg cga tcg caa tcc att tat Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr 20 25 30	96
ttc ctt ctc acg gat cga ttt gca agg acg gat ggg tcg acg act gcg Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala 35 40 45	144
act tgt aat act gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly 50 55 60	192
atc atc gac aag ttg gac tat atc cag gga atg ggc ttc aca gcc atc Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile 65 70 75 80	240
tgg atc acc ccc gtt aca gcc cag ctg ccc cag acc acc gca tat gga Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly 85 90 95	288
gat gcc tac cat ggc tac tgg cag cag gat ata tac tct ctg aac gaa Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu 100 105 110	336
aac tac ggc act gca gat gac ttg aag gcg ctc tct tcg gcc ctt cat Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His 115 120 125	384
gag agg ggg atg tat ctt atg gtc gat gtg gtt gct aac cat atg ggc Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly 130 135 140	432
tat gat gga gcg ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe 145 150 155 160	480
agt tcc caa gac tac ttc cac ccg ttc tgt ttc att caa aac tat gaa Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu 165 170 175	528
gat cag act cag gtt gag gat tgc tgg cta gga gat aac act gtc tcc Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser 180 185 190	576
ttg cct gat ctc gat acc acc aag gat gtg gtc aag aat gaa tgg tac Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr 195 200 205	624
gac tgg gtg gga tca ttg gta tcg aac tac tcc att gac ggc ctc cgt Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg 210 215 220	672

atc gac aca gta aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn 225 230 235 240	720
aaa gcc gca ggc gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro 245 250 255	768
gcc tac act tgt ccc tac cag aac gtc atg gac ggc gta ctg aac tat Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr 260 265 270	816
ccc att tac tat cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser 275 280 285	864
atg gac gac ctc tac aac atg atc aac acc gtc aaa tcc gac tgt cca Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro 290 295 300	912
gac tca aca ctc ctg ggc aca ttc gtc gag aac cac gac aac cca cg Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg 305 310 315 320	960
ttc gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala 325 330 335	1008
ttc atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu 340 345 350	1056
cag cac tac gcc ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp 355 360 365	1104
ctc tcg ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser 370 375 380	1152
gcg aac gca atc cgg aac tat gcc att agc aaa gat aca gga ttc gtg Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val 385 390 395 400	1200
acc tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met 405 410 415	1248
cgc aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys 420 425 430	1296
ggt gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr 435 440 445	1344

aca gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc acc gtg acg 1392
Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
450 455 460

gtt ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct 1440
Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
465 470 475 480

agg gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt 1488
Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
485 490 495

agc tcg tga 1497
Ser Ser

<210> 11
<211> 498
<212> PRT
<213> Aspergillus niger

<400> 11
Met Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala
1 5 10 15

Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr
20 25 30

Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
35 40 45

Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
50 55 60

Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
65 70 75 80

Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
85 90 95

Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
100 105 110

Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
115 120 125

Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
130 135 140

Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
145 150 155 160

Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
165 170 175

Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
180 185 190

Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
 195 200 205
 Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
 210 215 220
 Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
 225 230 235 240
 Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
 245 250 255
 Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
 260 265 270
 Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
 275 280 285
 Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
 290 295 300
 Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
 305 310 315 320
 Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
 325 330 335
 Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
 340 345 350
 Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
 355 360 365
 Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
 370 375 380
 Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
 385 390 395 400
 Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
 405 410 415
 Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
 420 425 430
 Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
 435 440 445
 Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
 450 455 460
 Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
 465 470 475 480
 Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
 485 490 495

Ser Ser

<210> 12

<211> 3697

<212> DNA

<213> Aspergillus niger

<400> 12

cttgtataac	gcttcctcaa	tgtcgtattt	cgaaaagaaaa	cgggctttct	ttatccaatc	60
cctgtggtaa	gattgatcgt	caggagatta	tctgcaggaa	acatcatggt	gggtaacca	120
aggttgtgtc	tgtataat	atacatgtaa	gatacatgag	cttcgggtat	ataatacaga	180
agtaccatac	agtaccgcgt	tatgaaaaca	cattaatccg	gatccttcc	tataatagac	240
tagcgtgctt	ggcatttaggg	ttcgaaaaac	aatcgaagag	tataagggga	tgacagcagt	300
aacgactcca	actgtacgcc	tccggtagt	agaccgagca	gccgagccag	ctcagcgcct	360
aaaacgcctt	atacaattaa	gcagttaaag	aagttagaat	ctacgcttaa	aaagctactt	420
aaaaatcgat	ctcgcagtcc	cgattcgcc	atcaaaaacca	gtttaaatca	actgattaaa	480
ggtgcgcgaa	gagctataaa	tgtatataaca	atattaaagc	attaattaga	gcaatatcag	540
gccgcgcacg	aaaggcaact	taaaaagcga	aagcgctcta	ctaaacagat	tactttgaa	600
aaaggcacat	cagtattaa	agcccgaatc	cttattaagc	gccgaaatca	ggcagataaa	660
gccatacagg	cagatagacc	tctacctatt	aaatcggctt	ctaggcgcgc	tccatctaaa	720
tgttctggct	gtgggttaca	ggggcataaa	attacgcact	acccgaatcg	atagaactac	780
tcattttat	atagaagtca	gaattcatgg	tgtttgatc	attttaaatt	tttatatggc	840
gggtgggtgg	caactcgctt	gcgcgggcaa	ctcgcttacc	gattacgtta	gggctgat	900
ttacgtaaaa	atcgtaagg	gatgcaagac	caaagtagta	aaacccccga	gtcaacagca	960
tccaagccca	agtccctcac	ggagaaaccc	cagcgtccac	atcacgagcg	aaggaccacc	1020
tctaggcattc	ggacgcacca	tccaaattaga	agcagcaaag	cgaaacagcc	caagaaaaag	1080
gtcggcccg	cggccttttc	tgcaacgctg	atcacggca	gcatccaac	caacaccctc	1140
cagagtact	aggggcccggaa	attaaagg	attaattcc	actcaaccac	aaatcacagt	1200
cgtccccgg	attgtcctgc	agaatgcaat	ttaaactctt	ctgcgaatcg	cttggattcc	1260
ccgccccctgg	ccgttagagct	taaagtatgt	cccttgcga	tgcgatgtat	cacaacat	1320
aaatactagc	aagggatgcc	atgcttggag	gatagcaacc	gacaacatca	catcaagctc	1380
tcccttctct	gaacaataaa	ccccacagaa	ggcatttatg	atggtcgcgt	ggtggctct	1440
atttctgtac	ggccttcagg	tcgcccacc	tgctttggct	gcaacgcctg	cgactggcg	1500
atcgcaatcc	atttatttcc	ttctcacgga	tcgatttgca	aggacggatg	ggtcgacgac	1560
tgcgacttgt	aatactgcgg	atcaggtgt	ttgttaccta	ctagcttca	gaaagaggaa	1620
tgtaaactga	cttgatata	aaatactgt	gtgaaacatg	gcagggcatc	atcgacaagg	1680
taaattgccc	ctttatcaaa	aaaaaagaag	gaaaagcaga	agaaaaataa	aataaaaaga	1740
actctagtcc	taaccatcac	atagttggac	tatatccagg	gaatgggctt	cacagccatc	1800
tggatcaccc	ccgttacagc	ccagctgccc	cagaccaccg	catatggaga	tgcctaccat	1860
ggctactggc	agcaggat	gtaagtcgt	ttctttaat	atctacctgt	catctttac	1920
atcaatatga	actaacttga	tggttttaga	tactctctga	acgaaaacta	cggcactgca	1980
gatgacttga	aggcgctctc	ttcgccccctt	catgagaggg	ggatgtatct	tatggtcgt	2040
gtgggttgc	accatatgg	tcgtggtcct	ttgcaactga	cttcgggtat	atggttcatt	2100
tcagttactga	caatgagtaa	tatcagggct	atgatggagc	gggtagctca	gtcgattaca	2160
gtgtgtttaa	accgttcagt	tcccaagact	acttccaccc	gttctgttcc	attcaaaact	2220
atgaagatca	gactcaggtt	gaggattgt	ggctaggaga	taacactgtc	tccttgccgt	2280
atctcgatac	caccaaggat	gtggtcaaga	atgaatggta	cgactgggt	ggatcattgg	2340
tatcgaacta	ctccagtaag	atatttctcc	ctcattctac	aacttggctg	atcgatgata	2400
cttacgaaat	cagttgacgg	cctccgtatc	gacacagtaa	aacacgtcca	gaaggacttc	2460
tggcccccgg	acaacaaagc	cgcaggcgt	tactgtatcg	gcgaggtgct	cgacgggtat	2520
ccggcctaca	cttgcctcta	ccagaacgtc	atggacggcg	tactgaacta	tcccattgtat	2580
ggttcctcca	accatgagcc	ttcttgcaag	tctcatctcc	taacgaaacg	gctaaaacca	2640
gttactatcc	actcctcaac	gccttcaagt	caaccccg	cagcatggac	gacctctaca	2700
acatgatcaa	caccgtcaaa	tccgactgtc	cagactcaac	actcctgggc	acattcgatcg	2760
agaaccacga	caacccacgg	ttcgcttcgt	aagtcttccc	tttattttc	cgttcccaat	2820

ttccacacag aaccccaccc aacaagagca aagttacacc aacgacatag ccctcgccaa	2880
gaacgtcgca gcattcatca tcctcaacga cggaatcccc atcatctacg ccggccaaga	2940
acagcaactac gccggcggaa acgaccccgc gaaccgcgaa gcaacctggc tctcgggcta	3000
cccgaccgac agcgagctgt acaagttaat tgcctccgcg aacgcaatcc ggaactatgc	3060
cattagcaaa gatacaggat tcgtgaccta caaggtaagc acaacctcta agcataccct	3120
aatggcctat cttagagta tctgacacaa gagactaatc actggcaata cagaactggc	3180
ccatctacaa agacgacaca acgatcgcca tgcgcaaggg cacagatggg tcgcagatcg	3240
tgactatctt gtccaacaag ggtgcttcgg gtgattcgta taccctctcc ttgagtggtg	3300
cgggttacac agccggccag caattgacgg aggtcattgg ctgcacgacc gtgacgggtg	3360
gttcggatgg aaatgtgcct gttcctatgg caggtggct acctaggta ttgtatccga	3420
ctgagaagtt ggcaggtgc aagatctgta gtagctcgta aagggtggag agtataatgat	3480
ggtactgcta ttcaatctgg cattggacag ttagtttgag tttgatgtac agttggagtc	3540
gttactgctg tcatccccctt atactcttcg attgttttc gaaccctaata gccaaggacag	3600
ctagtctatt ataggaaagg atccggatta atgtgtttc ataacgcggt actgtatggt	3660
acttctgtat tatatcaccg aagctcatgt atcttac	3697

<210> 13
 <211> 1497
 <212> DNA
 <213> Aspergillus niger

<220>
 <221> CDS
 <222> (1)..(1497)

<400> 13	
atg gtc gcg tgg tgg tct cta ttt ctg tac ggc ctt cag gtc gcg gca	48
Met Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala	
1 5 10 15	
cct gct ttg gct gca acg cct gcg gac tgg cga tcg caa tcc att tat	96
Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr	
20 25 30	
ttc ctt ctc acg gat cga ttt gca agg acg gat ggg tcg acg act gcg	144
Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala	
35 40 45	
act tgt aat act gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc	192
Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly	
50 55 60	
atc atc gac aag ttg gac tat atc cag gga atg ggc ttc aca gcc atc	240
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile	
65 70 75 80	
tgg atc acc ccc gtt aca gcc cag ctg ccc cag acc acc gca tat gga	288
Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly	
85 90 95	
gat gcc tac cat ggc tac tgg cag cag gat ata tac tct ctg aac gaa	336
Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu	
100 105 110	

aac tac ggc act gca gat gac ttg aag gcg ctc tct tcg gcc ctt cat Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His 115 120 125	384
gag agg ggg atg tat ctt atg gtc gat gtg gtt gct aac cat atg ggc Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly 130 135 140	432
tat gat gga gcg ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe 145 150 155 160	480
agt tcc caa gac tac ttc cac ccg ttc tgt ttc att caa aac tat gaa Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu 165 170 175	528
gat cag act cag gtt gag gat tgc tgg cta gga gat aac act gtc tcc Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser 180 185 190	576
ttg cct gat ctc gat acc acc aag gat gtg gtc aag aat gaa tgg tac Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr 195 200 205	624
gac tgg gtg gga tca ttg gta tcg aac tac tcc att gac ggc ctc cgt Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg 210 215 220	672
atc gac aca gta aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn 225 230 235 240	720
aaa gcc gca ggc gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro 245 250 255	768
gcc tac act tgt ccc tac cag aac gtc atg gac ggc gta ctg aac tat Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr 260 265 270	816
ccc att tac tat cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser 275 280 285	864
atg gac gac ctc tac aac atg atc aac acc gtc aaa tcc gac tgt cca Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro 290 295 300	912
gac tca aca ctc ctg ggc aca ttc gtc gag aac cac gac aac cca cgg Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg 305 310 315 320	960
ttc gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala 325 330 335	1008

ttc atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu 340 345 350	1056
cag cac tac gcc ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp 355 360 365	1104
ctc tcg ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser 370 375 380	1152
gcg aac gca atc cgg aac tat gcc att agc aaa gat aca gga ttc gtg Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val 385 390 395 400	1200
acc tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met 405 410 415	1248
cgc aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys 420 425 430	1296
ggt gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr 435 440 445	1344
aca gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr 450 455 460	1392
gtt ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro 465 470 475 480	1440
agg gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser 485 490 495	1488
agc tcg tga Ser Ser	1497

<210> 14
 <211> 498
 <212> PRT
 <213> Aspergillus niger

<400> 14
 Met Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala
 1 5 10 15
 Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr
 20 25 30

Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
 35 40 45
 Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
 50 55 60
 Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
 65 70 75 80
 Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
 85 90 95
 Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
 100 105 110
 Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
 115 120 125
 Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
 130 135 140
 Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
 145 150 155 160
 Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
 165 170 175
 Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
 180 185 190
 Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
 195 200 205
 Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
 210 215 220
 Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
 225 230 235 240
 Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
 245 250 255
 Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
 260 265 270
 Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
 275 280 285
 Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
 290 295 300
 Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
 305 310 315 320
 Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
 325 330 335

Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
 340 345 350
 Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
 355 360 365
 Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
 370 375 380
 Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
 385 390 395 400
 Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
 405 410 . 415
 Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
 420 425 430
 Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
 435 440 445
 Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
 450 455 460
 Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
 465 470 475 480
 Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
 485 490 495
 Ser Ser

<210> 15
 <211> 3570
 <212> DNA
 <213> Aspergillus niger

<400> 15
 ggaaccagta cggcagctga tagtatccga aagctgcaaa ttgcttcattc gaggctggca 60
 ttcgatagaa gaaagaatta tagacaacta gtcttgcaat atgacaattc tctttgatta 120
 ataaatgaaa gcacgcattgt atcagcctaa tagccgagtgc gccccatct ctggcggcct 180
 cccgagcagc gtggaatgcg tccaagatcc cgtccgcggg tcgtccttcg gtcggaaatga 240
 tgactggagc agcagacatgt gtcctgagct gaatgcattgt gatattcaca ttccagggag 300
 aattgtcggc tatttagaac cctctcggtt taaaagccct attagactat gggtgcgctc 360
 aagccactag ccagggatatc ccgctgaacg ctccatcacc ttgcagctga agtgcacat 420
 gggacgggct ttaacttttc gtagatataa gtttaattta tcctctccac acccataagg 480
 tcgtatggtg tcaaccgggt tagtctgcag gatttcattct cgcttcggca agcgaggcgc 540
 cctaacgggc agcctgcagc ttaccctgtt aaccccggtt caccaccccc cgagcaatcc 600
 gtcgcgtcct ccacgagtca taacaagggtt cggcggttgt ttcttacccc cactatcagg 660
 cgtattcagt taacagtca tagtcccgtg tcggagattt gttgttctgc aacaattaaa 720
 ggggaccagg gttaaatcct ggccccggaa ctgatcgag tttcgccaa tgagagatgt 780
 tgtatacccg cgttcctggc agatggatta attgcccgtt ccattggca tccatcaagc 840
 atcatacggg attagaagg tagttcgtgg gttgatctgc cgtgcaaggt gctcaaggct 900
 ctggagtcgt gctgaacgc aatatttaag aatcgtcgtc agggacagcg ttctctggat 960
 agtcaagctg tgcttggac gctgttctgt cgctttgtca aaacataatt cgcagcgtg 1020
 agattatcga ctgcgtctct 1080

ctgtcggtcg cagaatggcg cactcagtcg atttacttcc tattgacgga tcggttcggt	1140
aggacggaca attcgacgac agctacatgc gatacgggtg accaagtacg ttggattgc	1200
aggacttcca tcattcatct actgacttga atagatctat tgtggtgca gttggcaagg	1260
aatcatcaac catgttgtg atcaacttcat actatccgct gtgcgcgtgt ctgactttat	1320
ttgctgcagc tggattatat ccagggcatg ggattcacgg ccatctggat ctgcctatc	1380
actgaacagc tgccccagga tactgctgat ggtgaagctt accatggata ttggcagcag	1440
aagatgtatg cgctcctcct tcccatatcg taggctact ctcaggcggc gactgacttg	1500
acagatacga cgtgaactcc aacttcggca ctgcagatga cctcaagtcc ctctcagatg	1560
cgcttcatgc ccgcggaatg tacctcatgg tggacgtcgt ccctaaccac atggtaagtg	1620
ctgcttcagc atccttatca gtgaactcca agtgcacacg ctaactgtac cagggctacg	1680
ccggcaacgg caacgatgta gactacagcg tcttcgaccc cttcgattcc tcctcctact	1740
tccacccata ctgcctgatc acagattggg acaacttgc acatggtccaa gattgttggg	1800
agggtgacac catcgatct ctgccagacc taaacaccac cgaaactgcc gtgagaacaa	1860
tctggtatga ctggtagcc gacctggat ccaattattc aggtgcgaat tccaacccaa	1920
tttaaaataa ccatatacta agtgaatca ccagtcgacg gactccgcat cgacagtgtc	1980
ctcgaagtgc aaccagactt ctccccggc taccaggaag cagcaggtgt ctactgcgtc	2040
ggcgaagtgc acaacggcaa ccctgcctc gactgccat accagaaggt cctggacggc	2100
gtcctcaact atccgatgta catcccccta tacattgtt attagatctt cgctaactcc	2160
aaccagctac tggcaactcc tctacgcctt cgaatcctcc agcggcagca tcagcaacct	2220
ctacaacatg atcaaatccg tcgcaagcga ctgctccgat ccgacactac tcggcaactt	2280
catcgaaaac cacgacaatc cccgttgc ctcgtatgtc ccacccctc ccctccctac	2340
aatcacactc actaatacat ctaacagcta cacctccgac tactcgcaag ccaaaaacgt	2400
cctcagctac atttcctct ccgacggcat cccatcgtc tacgcccggc aagaacagca	2460
ctactccggc ggcaaggtgc cctacaacccg cgaagcgacc tggcttcag gctacgacac	2520
ctcccgagag ctgtacaccc ggatagccac cacgaacgcg atccgcaaac tagccatctc	2580
agctgactcg gcctacatta cctacgcgtt tcgtccttcc ctcccacccct ttaccccca	2640
ccctacaaac atccacata ctaacaacat ttcaataatg aaatagaatg atgcattcta	2700
cactgacagc aacaccatcg caatgcgcaa aggcaccta gggagccaa tcatcaccgt	2760
cctctccaac aaaggctcct caggaagcag ctacaccctg accctcagcg gaagcggcta	2820
cacatccggc acgaagctga tcgaagcgtc cacatgcaca tccgtgaccg tggactcgag	2880
cggcgatatt cccgtgccga tggcgtcggtt attaccgaga gttcttctgc ccgcgtccgt	2940
cgtcgatagc tcttcgctct gtggcgggag cggaaagatta tacgtcgagt aatccggagt	3000
ggtcggttac tgtacgttg ccgggtggga ccactttcga gtataagttt attaagggtgg	3060
agtcggatgg gactgttact tggaaaagtg attcgaatcg ggagtatacg gtgccggagt	3120
gtgggagtgg ggagacgggtg gttgatactt ggaggttagat gatctgagat ttctaagtgt	3180
gatgagggtg gttttgggt atgttagttt gcctttggta gtgttgggtt gggttgggtt	3240
aataattatg ttattgttt tggtgcttgc gaccatggat ttgaagtgaa aattttagg	3300
ggctacggaa gtgtattgtg gacatgtgag taaattcatc tgggtatgta caaagtgggt	3360
tagccagtgg gcttgaagaa aagtctcctg ggtctctggt ttgagtaccc atgttaagat	3420
caagcataaa aacatgaaat attggaaaaa caaagggtat ttaacaactc gtgagcatta	3480
gctcctgggt agaatgcaat cataacagaa agtacagcca ggcgtgtgtc ataaagaagt	3540
ccagttggga aacgaaagac tagaatcaaa	3570

<210> 16
 <211> 1518
 <212> DNA
 <213> *Aspergillus niger*

<220>
 <221> CDS
 <222> (1)..(1518)

<400> 16
 atg aga tta tcg act tcg agt ctc ttc ctt tcc gtg tct ctg ctg ggg
 Met Arg Leu Ser Thr Ser Ser Leu Phe Leu Ser Val Ser Leu Leu Gly
 1 5 10 15

48

aag	ctg	gcc	ctc	ggg	ctg	tcg	gct	gca	gaa	tgg	cgc	act	cag	tcg	att	96
Lys	Leu	Ala	Leu	Gly	Leu	Ser	Ala	Ala	Glu	Trp	Arg	Thr	Gln	Ser	Ile	
20							25						30			
tac	tcc	cta	ttg	acg	gat	cg	tcc	ggt	agg	acg	gac	aat	tcg	acg	aca	144
Tyr	Phe	Leu	Leu	Thr	Asp	Arg	Phe	Gly	Arg	Thr	Asp	Asn	Ser	Thr	Thr	
35							40						45			
gct	aca	tgc	gat	acg	ggt	gac	caa	atc	tat	tgt	ggt	ggc	agt	tgg	caa	192
Ala	Thr	Cys	Asp	Thr	Gly	Asp	Gln	Ile	Tyr	Cys	Gly	Gly	Ser	Trp	Gln	
50							55					60				
gga	atc	atc	aac	cat	ctg	gat	tat	atc	cag	ggc	atg	gga	tcc	acg	gcc	240
Gly	Ile	Ile	Asn	His	Leu	Asp	Tyr	Ile	Gln	Gly	Met	Gly	Phe	Thr	Ala	
65							70				75		80			
atc	tgg	atc	tcg	cct	atc	act	gaa	cag	ctg	ccc	cag	gat	act	gct	gat	288
Ile	Trp	Ile	Ser	Pro	Ile	Thr	Glu	Gln	Leu	Pro	Gln	Asp	Thr	Ala	Asp	
85							90					95				
ggt	gaa	gct	tac	cat	gga	tat	tgg	cag	cag	aag	ata	ta	cac	gtg	aac	336
Gly	Glu	Ala	Tyr	His	Gly	Tyr	Trp	Gln	Gln	Lys	Ile	Tyr	Asp	Val	Asn	
100							105					110				
tcc	aac	tcc	ggc	act	gca	gat	gac	ctc	aag	tcc	ctc	tca	gat	gcg	ctt	384
Ser	Asn	Phe	Gly	Thr	Ala	Asp	Asp	Leu	Lys	Ser	Leu	Ser	Asp	Ala	Leu	
115							120					125				
cat	gcc	cgc	gga	atg	tac	ctc	atg	gtg	gac	gtc	gtc	cct	aac	cac	atg	432
His	Ala	Arg	Gly	Met	Tyr	Leu	Met	Val	Asp	Val	Val	Pro	Asn	His	Met	
130							135					140				
ggc	tac	gcc	ggc	aac	ggc	aac	gat	gta	gac	tac	agc	gtc	tcc	gac	ccc	480
Gly	Tyr	Ala	Gly	Asn	Gly	Asn	Asp	Val	Asp	Tyr	Ser	Val	Phe	Asp	Pro	
145							150				155		160			
ttc	gat	tcc	tcc	tac	ttc	cac	cca	tac	tgc	ctg	atc	aca	gat	tgg		528
Phe	Asp	Ser	Ser	Tyr	Phe	His	Pro	Tyr	Cys	Leu	Ile	Thr	Asp	Trp		
165							170					175				
gac	aac	ttg	acc	atg	gtc	caa	gat	tgt	tgg	gag	ggt	gac	acc	atc	gta	576
Asp	Asn	Leu	Thr	Met	Val	Gln	Asp	Cys	Trp	Glu	Gly	Asp	Thr	Ile	Val	
180							185					190				
tct	ctg	cca	gac	cta	aac	acc	acc	gaa	act	gcc	gtg	aga	aca	atc	tgg	624
Ser	Leu	Pro	Asp	Leu	Asn	Thr	Thr	Glu	Thr	Ala	Val	Arg	Thr	Ile	Trp	
195							200					205				
tat	gac	tgg	gta	gcc	gac	ctg	gta	tcc	aat	tat	tca	gtc	gac	gga	ctc	672
Tyr	Asp	Trp	Val	Ala	Asp	Leu	Val	Ser	Asn	Tyr	Ser	Val	Asp	Gly	Leu	
210							215					220				
cgc	atc	gac	agt	gtc	ctc	gaa	gtc	gaa	cca	gac	ttc	ttc	ccg	ggc	tac	720
Arg	Ile	Asp	Ser	Val	Leu	Glu	Val	Glu	Pro	Asp	Phe	Phe	Pro	Gly	Tyr	
225							230				235		240			

cag gaa gca gca ggt gtc tac tgc gtc ggc gaa gtc gac aac ggc aac Gln Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn 245 250 255	768
cct gcc ctc gac tgc cca tac cag aag gtc ctg gac ggc gtc ctc aac Pro Ala Leu Asp Cys Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn 260 265 270	816
tat ccg atc tac tgg caa ctc ctc tac gcc ttc gaa tcc tcc agc ggc Tyr Pro Ile Tyr Trp Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly 275 280 285	864
agc atc agc aac ctc tac aac atg atc aaa tcc gtc gca agc gac tgc Ser Ile Ser Asn Leu Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys 290 295 300	912
tcc gat ccg aca cta ctc ggc aac ttc atc gaa aac cac gac aat ccc Ser Asp Pro Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro 305 310 315 320	960
cgt ttc gcc tcc tac acc tcc gac tac tcg caa gcc aaa aac gtc ctc Arg Phe Ala Ser Tyr Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu 325 330 335	1008
agc tac atc ttc ctc tcc gac ggc atc ccc atc gtc tac gcc ggc gaa Ser Tyr Ile Phe Leu Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu 340 345 350	1056
gaa cag cac tac tcc ggc ggc aag gtg ccc tac aac cgc gaa gcg acc Glu Gln His Tyr Ser Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr 355 360 365	1104
tgg ctt tca ggc tac gac acc tcc gca gag ctg tac acc tgg ata gcc Trp Leu Ser Gly Tyr Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala 370 375 380	1152
acc acg aac gcg atc cgc aaa cta gcc atc tca gct gac tcg gcc tac Thr Thr Asn Ala Ile Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr 385 390 395 400	1200
att acc tac gcg aat gat gca ttc tac act gac agc aac acc atc gca Ile Thr Tyr Ala Asn Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala 405 410 415	1248
atg cgc aaa ggc acc tca ggg agc caa gtc atc acc gtc ctc tcc aac Met Arg Lys Gly Thr Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn 420 425 430	1296
aaa ggc tcc tca gga agc agc tac acc ctg acc ctc agc gga agc ggc Lys Gly Ser Ser Gly Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly 435 440 445	1344
tac aca tcc ggc acg aag ctg atc gaa gcg tac aca tgc aca tcc gtg Tyr Thr Ser Gly Thr Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val 450 455 460	1392

acc gtg gac tcg agc ggc gat att ccc gtg ccg atg gcg tcg gga tta	1440
Thr Val Asp Ser Ser Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu	
465 470 475 480	
ccg aga gtt ctt ctg ccc gcg tcc gtc gtc gat agc tct tcg ctc tgt	1488
Pro Arg Val Leu Leu Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys	
485 490 495	
ggc ggg agc gga aga tta tac gtc gag taa	1518
Gly Gly Ser Gly Arg Leu Tyr Val Glu	
500 505	
<210> 17	
<211> 505	
<212> PRT	
<213> Aspergillus niger	
<400> 17	
Met Arg Leu Ser Thr Ser Ser Leu Phe Leu Ser Val Ser Leu Leu Gly	
1 5 10 15	
Lys Leu Ala Leu Gly Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile	
20 25 30	
Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr	
35 40 45	
Ala Thr Cys Asp Thr Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln	
50 55 60	
Gly Ile Ile Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala	
65 70 75 80	
Ile Trp Ile Ser Pro Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp	
85 90 95	
Gly Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn	
100 105 110	
Ser Asn Phe Gly Thr Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu	
115 120 125	
His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met	
130 135 140	
Gly Tyr Ala Gly Asn Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro	
145 150 155 160	
Phe Asp Ser Ser Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp	
165 170 175	
Asp Asn Leu Thr Met Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val	
180 185 190	
Ser Leu Pro Asp Leu Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp	
195 200 205	

Tyr Asp Trp Val Ala Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu
 210 215 220

Arg Ile Asp Ser Val Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr
 225 230 235 240

Gln Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn
 245 250 255

Pro Ala Leu Asp Cys Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn
 260 265 270

Tyr Pro Ile Tyr Trp Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly
 275 280 285

Ser Ile Ser Asn Leu Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys
 290 295 300

Ser Asp Pro Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro
 305 310 315 320

Arg Phe Ala Ser Tyr Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu
 325 330 335

Ser Tyr Ile Phe Leu Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu
 340 345 350

Glu Gln His Tyr Ser Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr
 355 360 365

Trp Leu Ser Gly Tyr Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala
 370 375 380

Thr Thr Asn Ala Ile Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr
 385 390 395 400

Ile Thr Tyr Ala Asn Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala
 405 410 415

Met Arg Lys Gly Thr Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn
 420 425 430

Lys Gly Ser Ser Gly Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly
 435 440 445

Tyr Thr Ser Gly Thr Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val
 450 455 460

Thr Val Asp Ser Ser Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu
 465 470 475 480

Pro Arg Val Leu Leu Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys
 485 490 495

Gly Gly Ser Gly Arg Leu Tyr Val Glu
 500 505

<210> 18
 <211> 2935
 <212> DNA
 <213> Penicillium chrysogenum

<400> 18		
ggttcgaaga ggccaagata ttatatcgag gagtagagca aaaataatgc tgatatatta	60	
atgaagagat gacaattccg acttccaact tccaaacttgg acctcggagt tggtgaatcc	120	
ggtcctgctt gccccatata gcttccgacc accggattt gaccaatcaa cgcaagaaaga	180	
tgtcagcagc ttcagggatc agcgtcacct gacccgttg ttgcccgtt caacgagcgc	240	
gtctcaatga tacttttagac ttgattaatt tacaccttt aatatttcca atctcccgag	300	
gatacctact tcgtaacaat gggtgaagat agctacacgc gcgaggagga gaattacgag	360	
gatgaagagc tcgacgagac cgtgagtatc aaaagtttga gatatagtta ccgattgttgc	420	
acggttgcct acatagagct tcaaataatcgt caaagatgcg gtgctgttt ctatagat	480	
tagcagttcg atgctcacgc ctcgtccatc gcctgatcct aagaaacatg gagacgaatc	540	
acccgcgtct gcagcttga agtgtgcata ccatctgatg caacaacgca tcatactccaa	600	
ccctcatgac atgattggcg tttgcttta cggAACGCAA tcttccaagt tctatgtga	660	
aaatgaggat gaccgtggag atctctcata tcctcactgt tatctgtaca cggatcttga	720	
tgttccatca gcccaggaag tcaagcaact gcgggtccctc gcatctccag cagatgctga	780	
tgtatgacgta ctgcaagttt tggagccatc aaaggagcca gcctccatgg ccaacatgct	840	
tttctgcgcc aaccaaataatc ttacctcaaa agctccaaac tttgcttctc gacgcctgtt	900	
tgtcgtgacc gacaacgata atccccacgc agacaacaaa ggaatgcggc ctgctgcaac	960	
agttcgtgcg agggacttgc acgatcttgg tgtcaatatc gagttgtttc ccatatctca	1020	
accagaccac gaattcgaca cctctaaatt ctacgacgta ggtcattaac cttgatttgc	1080	
taggggtata ctcacaattt gcaggacatt atctacaaaaa catcgccag tggatggagat	1140	
gcccctgcata acctacagcc ggataccaa acatcaacag ctaaaggcga tggactttca	1200	
ttgctcaatt ctctgttgc gaggatcaac tcacgatctg tccccggccg atcgctgttc	1260	
tcaaataatgtgc cacttggat cggacctaatt ttcacaaatccat ccgtcaatgg atatttgc	1320	
ctcaagaaac aagagcctgc aaggagttgc ttgtctggc aaggaggcga gactgctcag	1380	
attgccaag gagtcacaac tctaataatgtct gatgacacag ggcaggagat tgagaagtct	1440	
gacattcgca aggatcacaat gtttgggtggc gagcaggat cattcaccat cgaagaacaa	1500	
caggcgctaa gaagcttcgg tgacccgggtg atccgttata ttgggttcaa gccactgtca	1560	
gcccctccgt tctggggccaa tgtcaagcac ccctcgatcc ttatccctc tgaagaggac	1620	
tacgtcggtt caacaagagt cttttctgca ctgcatacaga aactcctcga atcggagaaa	1680	
ctggctttgg tctgggttcat ccccccgcaga aatgcctcac cagtcttagc tgctatgtatt	1740	
gcaggtgctg agaagatcga cgagaatggc gtgcagaaaa ttccacctgg gatgtggatt	1800	
atccctcttc ctttcgcaga tggatgtgcgc caaaatccag agagcaccgt ccaccggcga	1860	
ggagatgcgc tgaacgacgc catgcgagat gttgtcgcc agttgcagct ccccaaggct	1920	
gtgtacgatc cttcaaaaata tccgaatcct tggatgtgcgc cgtcaatcata atctttggga	1980	
caatgataact gactgattcg cagcgcttca atggcattat cgtatcttac aggctatcgc	2040	
cttggatgaa gatttcccag aatcaccaga tgacaagacc gtgcctaagt accgacaggt	2100	
tcacaaggat ggctgcttcc atgatcccaat aaatgcccga acgtactgac caaatggatg	2160	
ttctagcgcg ctggcgacta tattcttgcg tggccgagg aactgaaatt gcaagcctcc	2220	
gagatgtttg gtgggtcagt agccgcccacc tctacgctgg taaagcgagg tgccaagacc	2280	
gaggcagctg gtgagcaccat atcaaaggcg gtgaagggtt aagacagtga gcccggagt	2340	
gaagacgaag tgaagaaatg ctatgcgaaa ggcactgtt ccaaggtgag cattcaaatt	2400	
ctcccaggtt attgaccaaa ctaataactcg ctttcagctt acgggtggccg tgctgaagga	2460	
attcttgcata gcacatggcc gtgtacacgc agaaaagaaaa gcaatctcg tggaccgagt	2520	
tgagcagtac tttgagcaga agttttaaac attgatttgc agtttgctca ggatcgctt	2580	
gggggtggtcc aagggtgctg taatctgcgg cccgttaat gagttatgag tggatccatc	2640	
ttgcctgttt ccataaggatc atagtcattt caaatgaatc gatatctttt atccaggat	2700	
atgttaggaa cattatataat aagaatatac cggcgatcc ttttcgtatgt ctttcagat	2760	
gtatacaag ggcgaagccg gtaaaaggcg tgaacgcctt gatataatc accgatactt	2820	
ctttatgcaa aatgcccagaa aatacctcta gcaactacag ggtagaaaaa agagatcacc	2880	
cttccaaggat tggccttagtc ttccatgata gccttctccg atagtcactt catac	2935	

<210> 19
<211> 1977
<212> DNA
<213> *Penicillium chrysogenum*

<220>
<221> CDS
<222> (1)..(1977)

<400> 19
atg gtt gaa gat agc tac acg cgc gag gag gag aat tac gag gat gaa 48
Met Val Glu Asp Ser Tyr Thr Arg Glu Glu Asn Tyr Glu Asp Glu
1 5 10 15

gag ctc gac gag acc agc ttc aaa tca gtc aaa gat gcg gtg ctg ttt 96
Glu Leu Asp Glu Thr Ser Phe Lys Ser Val Lys Asp Ala Val Leu Phe
20 25 30

gct ata gat att agc agt tcg atg ctc acg cct cgt cca tcg cct gat 144
Ala Ile Asp Ile Ser Ser Met Leu Thr Pro Arg Pro Ser Pro Asp
35 40 45

cct aag aaa cat gga gac gaa tca ccc gcg tct gca gct ttg aag tgt 192
Pro Lys Lys His Gly Asp Glu Ser Pro Ala Ser Ala Ala Leu Lys Cys
50 55 60

gca tac cat ctg atgcaa cca cgc atc atc tcc aac cct cat gac atg 240
Ala Tyr His Leu Met Gln Gln Arg Ile Ile Ser Asn Pro His Asp Met
65 70 75 80

att ggc gtt ttg ctt tac gga acg caa tct tcc aag ttc tat gat gaa 288
Ile Gly Val Leu Leu Tyr Gly Thr Gln Ser Ser Lys Phe Tyr Asp Glu
85 90 95

aat gag gat gac cgt gga gat ctc tca tat cct cac tgt tat ctg tac 336
Asn Glu Asp Asp Arg Gly Asp Leu Ser Tyr Pro His Cys Tyr Leu Tyr
100 105 110

acg gat ctt gat gtt cca tca gcc cag gaa gtc aag caa ctg cggt tcc 384
Thr Asp Leu Asp Val Pro Ser Ala Gln Glu Val Lys Gln Leu Arg Ser
115 120 125

ctc gca tct cca gca gat gct gat gac gta ctg caa gtt ttg gag 432
Leu Ala Ser Pro Ala Asp Ala Asp Asp Val Leu Gln Val Leu Glu
130 135 140

cca tca aag gag cca gcc tcc atg gcc aac atg ctt ttc tgc gcc aac 480
Pro Ser Lys Glu Pro Ala Ser Met Ala Asn Met Leu Phe Cys Ala Asn
145 150 155 160

caa atc ttt acc tca aaa gct cca aac ttt gct tct cga cgc ctg ttt 528
Gln Ile Phe Thr Ser Lys Ala Pro Asn Phe Ala Ser Arg Arg Leu Phe
165 170 175

gtc gtg acc gac aac gat aat ccc cac gca gac aac aaa gga atg cgg			576
Val Val Thr Asp Asn Asp Asn Pro His Ala Asp Asn Lys Gly Met Arg			
180	185	190	
tct gct gca aca gtt cgt gcg agg gac ttg tac gat ctt ggt gtc aat			624
Ser Ala Ala Thr Val Arg Ala Arg Asp Leu Tyr Asp Leu Gly Val Asn			
195	200	205	
atc gag ttg ttt ccc ata tct caa cca gac cac gaa ttc gac acc tct			672
Ile Glu Leu Phe Pro Ile Ser Gln Pro Asp His Glu Phe Asp Thr Ser			
210	215	220	
aaa ttc tac gac gac att atc tac aaa aca tcg ccc agt gat gga gat			720
Lys Phe Tyr Asp Asp Ile Ile Tyr Lys Thr Ser Pro Ser Asp Gly Asp			
225	230	235	240
gcc cct gca tac cta cag ccg gat acc aac aca tca aca gct aaa ggc			768
Ala Pro Ala Tyr Leu Gln Pro Asp Thr Asn Thr Ser Thr Ala Lys Gly			
245	250	255	
gat gga ctt tca ttg ctc aat tct ctg ttg tcg agc atc aac tca cga			816
Asp Gly Leu Ser Leu Leu Asn Ser Leu Leu Ser Ser Ile Asn Ser Arg			
260	265	270	
tct gtc ccc cgc cga tcg ctg ttc tca aat gtg cca ctt gag atc gga			864
Ser Val Pro Arg Arg Ser Leu Phe Ser Asn Val Pro Leu Glu Ile Gly			
275	280	285	
cct aat ttc aaa ata tcc gtc aat gga tat ttg ctt ctc aag aaa caa			912
Pro Asn Phe Lys Ile Ser Val Asn Gly Tyr Leu Leu Leu Lys Lys Gln			
290	295	300	
gag cct gca agg agt tgc ttc gtc tgg caa gga ggc gag act gct cag			960
Glu Pro Ala Arg Ser Cys Phe Val Trp Gln Gly Gly Glu Thr Ala Gln			
305	310	315	320
att gcc aaa gga gtc aca act cta atg tct gat gac aca ggg cag gag			1008
Ile Ala Lys Gly Val Thr Leu Met Ser Asp Asp Thr Gly Gln Glu			
325	330	335	
att gag aag tct gac att cgc aag gca tac aag ttt ggt ggc gag cag			1056
Ile Glu Lys Ser Asp Ile Arg Lys Ala Tyr Lys Phe Gly Gly Glu Gln			
340	345	350	
gta tca ttc acc atc gaa gaa caa cag gcg cta aga agc ttc ggt gac			1104
Val Ser Phe Thr Ile Glu Glu Gln Gln Ala Leu Arg Ser Phe Gly Asp			
355	360	365	
ccg gtg atc cgt att att ggg ttc aag cca ctg tca gcc ctc ccg ttc			1152
Pro Val Ile Arg Ile Ile Gly Phe Lys Pro Leu Ser Ala Leu Pro Phe			
370	375	380	
tgg gcc aat gtc aag cac ccc tcg ttt att tat ccc tct gaa gag gac			1200
Trp Ala Asn Val Lys His Pro Ser Phe Ile Tyr Pro Ser Glu Glu Asp			
385	390	395	400

tac gtc ggt tca aca aga gtc ttt tct gca ctg cat cag aaa ctc ctc		1248
Tyr Val Gly Ser Thr Arg Val Phe Ser Ala Leu His Gln Lys Leu Leu		
405	410	415
gaa tcg gag aaa ctg gct ttg gtc tgg ttc atc ccc cgc aga aat gcc		1296
Glu Ser Glu Lys Leu Ala Leu Val Trp Phe Ile Pro Arg Arg Asn Ala		
420	425	430
tca cca gtc tta gct gct atg att gca ggt gct gag aag atc gac gag		1344
Ser Pro Val Leu Ala Ala Met Ile Ala Gly Ala Glu Lys Ile Asp Glu		
435	440	445
aat ggc gtg cag aaa att cca cct ggg atg tgg att atc cct ctt cct		1392
Asn Gly Val Gln Lys Ile Pro Pro Gly Met Trp Ile Ile Pro Leu Pro		
450	455	460
ttc gca gat gat gtg cgc caa aat cca gag agc acc gtc cac cgg gca		1440
Phe Ala Asp Asp Val Arg Gln Asn Pro Glu Ser Thr Val His Arg Ala		
465	470	475
480		
gga gat gcg ctg aac gac gcc atg cga gat gtt gtt cgc cag ttg cag		1488
Gly Asp Ala Leu Asn Asp Ala Met Arg Asp Val Val Arg Gln Leu Gln		
485	490	495
ctc ccc aag gct gtg tac gat cct tca aaa tat ccg aat cct tcg ctt		1536
Leu Pro Lys Ala Val Tyr Asp Pro Ser Lys Tyr Pro Asn Pro Ser Leu		
500	505	510
caa tgg cat tat cgt atc tta cag gct atc gcc ttg gat gaa gat ttc		1584
Gln Trp His Tyr Arg Ile Leu Gln Ala Ile Ala Leu Asp Glu Asp Phe		
515	520	525
cca gaa tca cca gat gac aag acc gtg cct aag tac cga cag gtt cac		1632
Pro Glu Ser Pro Asp Asp Lys Thr Val Pro Lys Tyr Arg Gln Val His		
530	535	540
aag gtt ggc tgc ttc cat gat ccc aga aat gcc cga aca tgg gcc gag		1680
Lys Val Gly Cys Phe His Asp Pro Arg Asn Ala Arg Thr Trp Ala Glu		
545	550	555
560		
gaa ctg aaa ttg caa gcc tcc gag atg ttt ggt ggg tca gta gcc gcc		1728
Glu Leu Lys Leu Gln Ala Ser Glu Met Phe Gly Gly Ser Val Ala Ala		
565	570	575
acc tct acg ctg gta aag cga ggt gcc aag acc gag gca gct ggt gag		1776
Thr Ser Thr Leu Val Lys Arg Gly Ala Lys Thr Glu Ala Ala Gly Glu		
580	585	590
cac cca tca aag cgg gtg aag gtt gaa gac agt gag ccc gga gtg gaa		1824
His Pro Ser Lys Arg Val Lys Val Glu Asp Ser Glu Pro Gly Val Glu		
595	600	605
gac gaa gtg aag aaa tgc tat gcg aaa ggc act gtt tcc aag ctt acg		1872
Asp Glu Val Lys Lys Cys Tyr Ala Lys Gly Thr Val Ser Lys Leu Thr		
610	615	620

gtg gcc gtg ctg aag gaa ttc ttg cat gca cat ggc cgt gct aca gca 1920
Val Ala Val Leu Lys Glu Phe Leu His Ala His Gly Arg Ala Thr Ala
625 630 635 640

gga aag aaa gca gat ctc gtg gac cga gtt gag cag tac ttt gag cag 1968
Gly Lys Lys Ala Asp Leu Val Asp Arg Val Glu Gln Tyr Phe Glu Gln
645 650 655

aag ttt taa 1977
Lys Phe

<210> 20
<211> 658
<212> PRT
<213> Penicillium chrysogenum

<400> 20
Met Val Glu Asp Ser Tyr Thr Arg Glu Glu Glu Asn Tyr Glu Asp Glu
1 5 10 15

Glu Leu Asp Glu Thr Ser Phe Lys Ser Val Lys Asp Ala Val Leu Phe
20 25 30

Ala Ile Asp Ile Ser Ser Ser Met Leu Thr Pro Arg Pro Ser Pro Asp
35 40 45

Pro Lys Lys His Gly Asp Glu Ser Pro Ala Ser Ala Ala Leu Lys Cys
50 55 60

Ala Tyr His Leu Met Gln Gln Arg Ile Ile Ser Asn Pro His Asp Met
65 70 75 80

Ile Gly Val Leu Leu Tyr Gly Thr Gln Ser Ser Lys Phe Tyr Asp Glu
85 90 95

Asn Glu Asp Asp Arg Gly Asp Leu Ser Tyr Pro His Cys Tyr Leu Tyr
100 105 110

Thr Asp Leu Asp Val Pro Ser Ala Gln Glu Val Lys Gln Leu Arg Ser
115 120 125

Leu Ala Ser Pro Ala Asp Ala Asp Asp Val Leu Gln Val Leu Glu
130 135 140

Pro Ser Lys Glu Pro Ala Ser Met Ala Asn Met Leu Phe Cys Ala Asn
145 150 155 160

Gln Ile Phe Thr Ser Lys Ala Pro Asn Phe Ala Ser Arg Arg Leu Phe
165 170 175

Val Val Thr Asp Asn Asp Asn Pro His Ala Asp Asn Lys Gly Met Arg
180 185 190

Ser Ala Ala Thr Val Arg Ala Arg Asp Leu Tyr Asp Leu Gly Val Asn
195 200 205

Ile Glu Leu Phe Pro Ile Ser Gln Pro Asp His Glu Phe Asp Thr Ser
 210 215 220
 Lys Phe Tyr Asp Asp Ile Ile Tyr Lys Thr Ser Pro Ser Asp Gly Asp
 225 230 235 240
 Ala Pro Ala Tyr Leu Gln Pro Asp Thr Asn Thr Ser Thr Ala Lys Gly
 245 250 255
 Asp Gly Leu Ser Leu Leu Asn Ser Leu Leu Ser Ser Ile Asn Ser Arg
 260 265 270
 Ser Val Pro Arg Arg Ser Leu Phe Ser Asn Val Pro Leu Glu Ile Gly
 275 280 285
 Pro Asn Phe Lys Ile Ser Val Asn Gly Tyr Leu Leu Lys Lys Gln
 290 295 300
 Glu Pro Ala Arg Ser Cys Phe Val Trp Gln Gly Gly Glu Thr Ala Gln
 305 310 315 320
 Ile Ala Lys Gly Val Thr Thr Leu Met Ser Asp Asp Thr Gly Gln Glu
 325 330 335
 Ile Glu Lys Ser Asp Ile Arg Lys Ala Tyr Lys Phe Gly Gly Glu Gln
 340 345 350
 Val Ser Phe Thr Ile Glu Glu Gln Ala Leu Arg Ser Phe Gly Asp
 355 360 365
 Pro Val Ile Arg Ile Ile Gly Phe Lys Pro Leu Ser Ala Leu Pro Phe
 370 375 380
 Trp Ala Asn Val Lys His Pro Ser Phe Ile Tyr Pro Ser Glu Glu Asp
 385 390 395 400
 Tyr Val Gly Ser Thr Arg Val Phe Ser Ala Leu His Gln Lys Leu Leu
 405 410 415
 Glu Ser Glu Lys Leu Ala Leu Val Trp Phe Ile Pro Arg Arg Asn Ala
 420 425 430
 Ser Pro Val Leu Ala Ala Met Ile Ala Gly Ala Glu Lys Ile Asp Glu
 435 440 445
 Asn Gly Val Gln Lys Ile Pro Pro Gly Met Trp Ile Ile Pro Leu Pro
 450 455 460
 Phe Ala Asp Asp Val Arg Gln Asn Pro Glu Ser Thr Val His Arg Ala
 465 470 475 480
 Gly Asp Ala Leu Asn Asp Ala Met Arg Asp Val Val Arg Gln Leu Gln
 485 490 495
 Leu Pro Lys Ala Val Tyr Asp Pro Ser Lys Tyr Pro Asn Pro Ser Leu
 500 505 510

Gln Trp His Tyr Arg Ile Leu Gln Ala Ile Ala Leu Asp Glu Asp Phe
515 520 525

Pro Glu Ser Pro Asp Asp Lys Thr Val Pro Lys Tyr Arg Gln Val His
530 535 540

Lys Val Gly Cys Phe His Asp Pro Arg Asn Ala Arg Thr Trp Ala Glu
545 550 555 560

Glu Leu Lys Leu Gln Ala Ser Glu Met Phe Gly Gly Ser Val Ala Ala
565 570 575

Thr Ser Thr Leu Val Lys Arg Gly Ala Lys Thr Glu Ala Ala Gly Glu
580 585 590

His Pro Ser Lys Arg Val Lys Val Glu Asp Ser Glu Pro Gly Val Glu
595 600 605

Asp Glu Val Lys Lys Cys Tyr Ala Lys Gly Thr Val Ser Lys Leu Thr
610 615 620

Val Ala Val Leu Lys Glu Phe Leu His Ala His Gly Arg Ala Thr Ala
625 630 635 640

Gly Lys Lys Ala Asp Leu Val Asp Arg Val Glu Gln Tyr Phe Glu Gln
645 650 655

Lys Phe

<210> 21

<211> 3605

<212> DNA

<213> Penicillium chrysogenum

<400> 21

gattcggat attttatgac ctaaggagag ttgagttggc gataaagtgc atgtgaagtt 60
gcatcgaggg gaagaagtgg cagttatcgc tacgatccaa ttcttaatga aagccttatt 120
tccacttcca aatagaggga gctggcttct aacgacgcac agaccaccaa acaccaacaa 180
agacggcgtg tcatgtcatg tgccttcgtg ttccggctca aaccgcaagt gggaaatatca 240
cgctctgcc ttttgtcttg agccccaaag caactttgtc ttgccatttt cccaaacatca 300
tcatcattat ggcggagaaa gaggctacag ttacattgt agacatggg cggcttatgg 360
gcgagcgcca ccatggccgt cctatgacag atctcgaatg ggccatgcag tatgtctggg 420
ataggatcac tgccacggta tgtgacttga ccttgttcaa cgccagagaa ctgacaattc 480
cagggtggcta ctggcgaaa gacggctacg gttggcgtag ttggactcag gactgatgg 540
gagttggcgg ctaccagtca gcacccattg ggacccttgt ctcatgtttg gaacagggaa 600
tatcaacgac ttgaaagaag agagctttc taatattct attctcttcg gtcttggcca 660
gtatgtgtgg ctttaattat cgacagctt atgccgagtc gcctgactaa attgtcttc 720
agagtcctca tgcctgatat ccggaaactg cgagaaacga tcaagcccac caacactaac 780
agaggcgatg gtatgtgact gttgaagtct tgtcaagctg cttattctga ctttatataa 840
gccatctctt ctattgtcat tgccatgcag atgatcattg actacacgaa gaaaaacaaa 900
tacaagcgca agatcatctt ggtgaccaat ggtaccggcg tgatgagcga tgataatatc 960
gaaggcatca ttgaaaagat gaaagagggtt aacattgagt tgggtgtcat gtatgtttct 1020
tgccgacatg acttcacatt catgctaata ctatgcagtg gagccgattt tgatgacgct 1080
gagttggtg taaaggaaga agacaaagac agtcgaaagg ttcttaagcca tctccaatct 1140
attctgttat tcatgttgac aaagcgctc gcaggctgaa aacgagactt ttctccgaag 1200

cctggctgag	gactgcgaag	gtgcttatgg	aacgctggag	caagccgtt	cgaaatttgg	1260
tattccccgt	atcaaagtga	ccaagagcat	gccatcttc	aaggaaacc	tcacgctcg	1320
caatcccgag	gagtatgaca	cggctatgac	tatacccg	gagcgatact	tccgaaccta	1380
cgtcgccaaa	ccaatctcg	cgagctcg	cgtaccacgc	tccggcaccg	aacctgaaag	1440
tcaagcaccg	gttaaaggcg	atgctgaagg	cgatgctctc	gcctcagtgc	gaacatcacg	1500
gacgtatcg	atcacagatg	agtccgcacc	aggtggtaag	atcgacgtt	aacgcgatga	1560
cctcgccaaag	gggtacgagt	acggacgtac	cgcggttc	atcgagcaa	ccgatgagaa	1620
tgttgcaaat	ctacaaacat	ttgctggat	ggggctgatc	gggttcgtt	agaaggatca	1680
ggtgtgtctt	tatgccaata	ttaagtgc	taacagctaa	tccgtgactt	agtatgaccg	1740
gtacatgcat	atgtcaaaca	cgaatatcat	catccctcg	cgtgcaaatg	actatgcgtc	1800
tcttgcgtt	tcttctctca	ttcatgcact	ctacgaattt	gagtcctatg	cggttgc	1860
cttggtgacc	aaagaatcca	aaccaccat	gcttgtgtt	ctagctccat	ctatcgaggc	1920
agactatgag	tgcttgattt	aagtacagct	tccatttgc	gaagacgtgc	ggtcgatcg	1980
gttcccac	ttggataaga	ttatcactgt	ctctggcaag	gtgggtact	aacatcgaaa	2040
cctcccaagc	gtggcgtt	aagatgcgt	gagtaactac	gtggacagca	tggattttgt	2100
caccacaaac	gacgaagggt	aagtatagtc	tacttgatta	tcgactttat	cagttaatca	2160
aaagagccag	gcaagccact	gacgatctcc	caatcgacga	gtcattctca	ccgttattgc	2220
accgcacatcg	atcagcagtt	cgatatcg	ctgtgcattcc	caatgaccct	gtcctcgacc	2280
cctcagagcg	gctcactgaa	ttcgacacc	cctcagaaga	catggtcaag	aactccaaat	2340
cccatcttga	gaaattgat	tccatagcag	atgtcaagaa	aggtaacctc	gattccata	2400
ctacatccgg	aagataccct	actcaccac	gcattttgtc	ttatagttcc	accgaagaca	2460
aaaggccgt	aacgccaacg	tgaaacagag	aaacctct	caggtttgg	cgtggacgccc	2520
ctgctcagcc	tcgaacccaa	gcgaacgaag	attccacc	agaatgcaat	cccagagttc	2580
aagcaaacac	tttcccgc	ggaaaacatc	gacgcaatcc	acgacgctgt	gcagcagatg	2640
gctaaaatca	tcgagagcca	gatcacacac	agcctcg	attcaaatta	cgaccgtt	2700
atcgaggggc	ttggtactat	gcgtgaagaa	ctggtgact	atgaggaacc	ggcgggt	2760
aatgactttg	tgcgtcagtt	gaagggcaag	atgttgc	aggagcttgg	tgggatcgg	2820
agggagctgt	ggtggttt	aaggaaggga	aagcttggc	tcattggcaa	gagtggatgt	2880
gatagctcg	ctgtt	gagga	gcaagaggct	caagaggta	ggtttggc	2940
aatggaacga	gtgcta	acac	tgcgtata	ttctggct	caattgagga	3000
ggggcgggtt	attgtctcg	tattcaa	tgaaatagt	agcatacgag	ggatgtggaa	3060
tattcata	attctctat	ccagatttac	gcgtatgt	gcttcctgt	gaagttatgt	3120
tatatgg	tac	gtcg	taaggccgg	aaacggagta	tagtccac	3180
ggtccaataa	tactgacc	ccagatcaa	ggatacg	tggaggg	acggagaaat	3240
ggaaatattt	agcaagcc	tgaacagcat	tgtcatatag	acgtagaatt	gacacatata	3300
ggaacgaagc	ccgcagacag	aacaatatga	ggcacga	gaatcggt	ccaattgca	3360
ggcatgacga	gtcgtcaat	aacaacagaa	ccaaacgccc	tgcataacat	gcccaataac	3420
cagtattcgc	tccagaaaac	agcaaaaagac	cgagatttgc	aaactcaa	attaaaaagc	3480
atccagatgc	atcagggaaa	aggggtatgc	agaagtgtt	tcccggt	acgagaagaa	3540
tggaacaaga	agcgctccga	ggaaacttgg	agagttcga	ggggcgaa	aagagagcag	3600
aacat						3605

<210> 22
 <211> 2157
 <212> DNA
 <213> *Penicillium chrysogenum*

<220>
 <221> CDS
 <222> (1)..(2157)

<400> 22
 atg gcg gag aaa gag gct aca gtt tac att gta gac atg gga cgg tct
 Met Ala Glu Lys Glu Ala Thr Val Tyr Ile Val Asp Met Gly Arg Ser
 1 5 10 15

48

atg ggc gag cgc cac cat ggc cgt cct atg aca gat ctc gaa tgg gcc	96
Met Gly Arg His His Gly Arg Pro Met Thr Asp Leu Glu Trp Ala	
20 25 30	
atg cag tat gtc tgg gat agg atc act gcc acg gtg gct act ggt cga	144
Met Gln Tyr Val Trp Asp Arg Ile Thr Ala Thr Val Ala Thr Gly Arg	
35 40 45	
aag acg gct acg gtt ggc gta gtt gga ctc agg act gat gtc agc acc	192
Lys Thr Ala Thr Val Gly Val Val Gly Leu Arg Thr Asp Val Ser Thr	
50 55 60	
cat tgg gac cct tgt ctc atg ttt gga aca gga act atc aac gac ttg	240
His Trp Asp Pro Cys Leu Met Phe Gly Thr Gly Thr Ile Asn Asp Leu	
65 70 75 80	
gaa gaa gag agc ttt tct aat att tct att ctc ttc ggt ctt ggc caa	288
Glu Glu Glu Ser Phe Ser Asn Ile Ser Ile Leu Phe Gly Leu Gly Gln	
85 90 95	
gtc ctc atg cct gat atc cgg aaa ctg cga gaa acg atc aag ccc agc	336
Val Leu Met Pro Asp Ile Arg Lys Leu Arg Glu Thr Ile Lys Pro Ser	
100 105 110	
aac act aac aga ggc gat gcc atc tct tct att gtc att gcc atg cag	384
Asn Thr Asn Arg Gly Asp Ala Ile Ser Ser Ile Val Ile Ala Met Gln	
115 120 125	
atg atc att gac tac acg aag aaa aac aaa tac aag cgc aag atc atc	432
Met Ile Ile Asp Tyr Thr Lys Lys Asn Lys Tyr Lys Arg Lys Ile Ile	
130 135 140	
ttg gtg acc aat ggt acc ggc gtg atg agc gat gat aat atc gaa ggc	480
Leu Val Thr Asn Gly Thr Gly Val Met Ser Asp Asp Asn Ile Glu Gly	
145 150 155 160	
atc att gaa aag atg aaa gag gtt aac att gag ttg gtg gtc atg tat	528
Ile Ile Glu Lys Met Lys Glu Val Asn Ile Glu Leu Val Val Met Tyr	
165 170 175	
tat ggt gta aag gaa gaa gac aaa gac agt cga aag gct gaa aac gag	576
Tyr Gly Val Lys Glu Glu Asp Lys Asp Ser Arg Lys Ala Glu Asn Glu	
180 185 190	
act ttt ctc cga agc ctg gct gag gac tgc gaa ggt gct tat gga acg	624
Thr Phe Leu Arg Ser Leu Ala Glu Asp Cys Glu Gly Ala Tyr Gly Thr	
195 200 205	
ctg gag caa gcc gtt tcg gaa ttg gat att ccc cgt atc aaa gtg acc	672
Leu Glu Gln Ala Val Ser Glu Leu Asp Ile Pro Arg Ile Lys Val Thr	
210 215 220	
aag agc atg cca tct ttc aag gga aac ctc acg ctc ggc aat ccc gag	720
Lys Ser Met Pro Ser Phe Lys Gly Asn Leu Thr Leu Gly Asn Pro Glu	
225 230 235 240	

gag tat gac acg gct atg act ata ccc gtg gag cga tac ttc cga acc Glu Tyr Asp Thr Ala Met Thr Ile Pro Val Glu Arg Tyr Phe Arg Thr 245 250 255	768
tac gtc gcc aaa cca atc tca gcg agc tcg ttc gta cca cgc tcc ggc Tyr Val Ala Lys Pro Ile Ser Ala Ser Ser Phe Val Pro Arg Ser Gly 260 265 270	816
acc gaa cct gga agt caa gca ccg gtt aaa ggc gat gct gaa ggc gat Thr Glu Pro Gly Ser Gln Ala Pro Val Lys Gly Asp Ala Glu Gly Asp 275 280 285	864
gct ctc gcc tca gtg cga aca tca cgg acg tat cag atc aca gat gag Ala Leu Ala Ser Val Arg Thr Ser Arg Thr Tyr Gln Ile Thr Asp Glu 290 295 300	912
tcc gca cca ggt ggt aag atc gac gtt gaa cgc gat gac ctc gcc aag Ser Ala Pro Gly Gly Lys Ile Asp Val Glu Arg Asp Asp Leu Ala Lys 305 310 315 320	960
ggg tac gag tac gga cgt acc gcg gtt cct atc gag caa acc gat gag Gly Tyr Glu Tyr Gly Arg Thr Ala Val Pro Ile Glu Gln Thr Asp Glu 325 330 335	1008
aat gtt gca aat cta caa aca ttt gct ggt atg ggg ctg atc ggg ttc Asn Val Ala Asn Leu Gln Thr Phe Ala Gly Met Gly Leu Ile Gly Phe 340 345 350	1056
gtt cag aag gat cag tat gac cgg tac atg cat atg tca aac acg aat Val Gln Lys Asp Gln Tyr Asp Arg Tyr Met His Met Ser Asn Thr Asn 355 360 365	1104
atc atc atc cct cag cgt gca aat gac tat gcg tct ctt gcg ttg tct Ile Ile Ile Pro Gln Arg Ala Asn Asp Tyr Ala Ser Leu Ala Leu Ser 370 375 380	1152
tct ctc att cat gca ctc tac gaa ttg gag tcc tat gcg gtt gcc cgc Ser Leu Ile His Ala Leu Tyr Glu Leu Glu Ser Tyr Ala Val Ala Arg 385 390 395 400	1200
ttg gtg acc aaa gaa tcc aaa cca ccg atg ctt gtg ttg cta gct cca Leu Val Thr Lys Glu Ser Lys Pro Pro Met Leu Val Leu Leu Ala Pro 405 410 415	1248
tct atc gag gca gac tat gag tgc ttg att gaa gta cag ctt cca ttt Ser Ile Glu Ala Asp Tyr Glu Cys Leu Ile Glu Val Gln Leu Pro Phe 420 425 430	1296
gca gaa gac gtg cgg tcg tat cgg ttc cca cct ttg gat aag att atc Ala Glu Asp Val Arg Ser Tyr Arg Phe Pro Pro Leu Asp Lys Ile Ile 435 440 445	1344
act gtc tct ggc aag gtg gtg act gaa cat cga aac ctc cca agc gtg Thr Val Ser Gly Lys Val Val Thr Glu His Arg Asn Leu Pro Ser Val 450 455 460	1392

gcg ttg aaa gat gcg atg agt aac tac gtg gac agc atg gat ttt gtc Ala Leu Lys Asp Ala Met Ser Asn Tyr Val Asp Ser Met Asp Phe Val 465 470 475 480	1440
acc aca aac gac gaa ggg caa gcc act gac gat ctc cca atc gac gag Thr Thr Asn Asp Glu Gly Gln Ala Thr Asp Asp Leu Pro Ile Asp Glu 485 490 495	1488
tca ttc tca ccg tta ttg cac cgc atc gaa tca gca gtt cga tat cgt Ser Phe Ser Pro Leu Leu His Arg Ile Glu Ser Ala Val Arg Tyr Arg 500 505 510	1536
gct gtg cat ccc aat gac cct gtc ctc gac ccc tca gag cgg ctc act Ala Val His Pro Asn Asp Pro Val Leu Asp Pro Ser Glu Arg Leu Thr 515 520 525	1584
gaa ttc gca cac ccc tca gaa gac atg gtc aag aac tcc aaa tcc cat Glu Phe Ala His Pro Ser Glu Asp Met Val Lys Asn Ser Lys Ser His 530 535 540	1632
ctt gag aaa ttg atg tcc ata gca gat gtc aag aaa gtt cca ccg aag Leu Glu Lys Leu Met Ser Ile Ala Asp Val Lys Lys Val Pro Pro Lys 545 550 555 560	1680
aca aaa ggc cgt aaa cgc caa cgt gaa aca gag aaa cct ctc tca ggt Thr Lys Gly Arg Lys Arg Gln Arg Glu Thr Glu Lys Pro Leu Ser Gly 565 570 575	1728
ttg gac gtg gac gcc ctg ctc agc ctc gaa ccc aag cga acg aag att Leu Asp Val Asp Ala Leu Leu Ser Leu Glu Pro Lys Arg Thr Lys Ile 580 585 590	1776
tcc acc gag aat gca atc cca gag ttc aag caa aca ctt tcc cgc gcg Ser Thr Glu Asn Ala Ile Pro Glu Phe Lys Gln Thr Leu Ser Arg Ala 595 600 605	1824
gaa aac atc gac gca atc cac gac gct gtg cag cag atg gct aaa atc Glu Asn Ile Asp Ala Ile His Asp Ala Val Gln Gln Met Ala Lys Ile 610 615 620	1872
atc gag agc cag atc aca cac agc ctc ggt cat tca aat tac gac cgt Ile Glu Ser Gln Ile Thr His Ser Leu Gly His Ser Asn Tyr Asp Arg 625 630 635 640	1920
gtt atc gag ggg ctt ggt act atg cgt gaa gaa ctg gtg gac tat gag Val Ile Glu Gly Leu Gly Thr Met Arg Glu Glu Leu Val Asp Tyr Glu 645 650 655	1968
gaa ccg gcg gtg tac aat gac ttt gtg cgt cag ttg aag ggc aag atg Glu Pro Ala Val Tyr Asn Asp Phe Val Arg Gln Leu Lys Gly Lys Met 660 665 670	2016
ttg cgg gag gag ctg ggt ggg gat cgg agg gag ctg tgg tgg ttt gta Leu Arg Glu Glu Leu Gly Gly Asp Arg Arg Glu Leu Trp Trp Phe Val 675 680 685	2064

agg aag gga aag ctt ggg ctc att ggc aag agt gag gtg gat agc tcg	2112
Arg Lys Gly Lys Leu Gly Leu Ile Gly Lys Ser Glu Val Asp Ser Ser	
690 695 700	
gct gtt gag gag caa gag gct caa gag ttt ctg gct ccc aat tga	2157
Ala Val Glu Glu Gln Glu Ala Gln Glu Phe Leu Ala Pro Asn	
705 710 715	
<210> 23	
<211> 718	
<212> PRT	
<213> Penicillium chrysogenum	
<400> 23	
Met Ala Glu Lys Glu Ala Thr Val Tyr Ile Val Asp Met Gly Arg Ser	
1 5 10 15	
Met Gly Glu Arg His His Gly Arg Pro Met Thr Asp Leu Glu Trp Ala	
20 25 30	
Met Gln Tyr Val Trp Asp Arg Ile Thr Ala Thr Val Ala Thr Gly Arg	
35 40 45	
Lys Thr Ala Thr Val Gly Val Val Gly Leu Arg Thr Asp Val Ser Thr	
50 55 60	
His Trp Asp Pro Cys Leu Met Phe Gly Thr Gly Thr Ile Asn Asp Leu	
65 70 75 80	
Glu Glu Glu Ser Phe Ser Asn Ile Ser Ile Leu Phe Gly Leu Gly Gln	
85 90 95	
Val Leu Met Pro Asp Ile Arg Lys Leu Arg Glu Thr Ile Lys Pro Ser	
100 105 110	
Asn Thr Asn Arg Gly Asp Ala Ile Ser Ser Ile Val Ile Ala Met Gln	
115 120 125	
Met Ile Ile Asp Tyr Thr Lys Lys Asn Lys Tyr Lys Arg Lys Ile Ile	
130 135 140	
Leu Val Thr Asn Gly Thr Gly Val Met Ser Asp Asp Asn Ile Glu Gly	
145 150 155 160	
Ile Ile Glu Lys Met Lys Glu Val Asn Ile Glu Leu Val Val Met Tyr	
165 170 175	
Tyr Gly Val Lys Glu Glu Asp Lys Asp Ser Arg Lys Ala Glu Asn Glu	
180 185 190	
Thr Phe Leu Arg Ser Leu Ala Glu Asp Cys Glu Gly Ala Tyr Gly Thr	
195 200 205	
Leu Glu Gln Ala Val Ser Glu Leu Asp Ile Pro Arg Ile Lys Val Thr	
210 215 220	

Lys Ser Met Pro Ser Phe Lys Gly Asn Leu Thr Leu Gly Asn Pro Glu
 225 230 235 240
 Glu Tyr Asp Thr Ala Met Thr Ile Pro Val Glu Arg Tyr Phe Arg Thr
 245 250 255
 Tyr Val Ala Lys Pro Ile Ser Ala Ser Ser Phe Val Pro Arg Ser Gly
 260 265 270
 Thr Glu Pro Gly Ser Gln Ala Pro Val Lys Gly Asp Ala Glu Gly Asp
 275 280 285
 Ala Leu Ala Ser Val Arg Thr Ser Arg Thr Tyr Gln Ile Thr Asp Glu
 290 295 300
 Ser Ala Pro Gly Gly Lys Ile Asp Val Glu Arg Asp Asp Leu Ala Lys
 305 310 315 320
 Gly Tyr Glu Tyr Gly Arg Thr Ala Val Pro Ile Glu Gln Thr Asp Glu
 325 330 335
 Asn Val Ala Asn Leu Gln Thr Phe Ala Gly Met Gly Leu Ile Gly Phe
 340 345 350
 Val Gln Lys Asp Gln Tyr Asp Arg Tyr Met His Met Ser Asn Thr Asn
 355 360 365
 Ile Ile Ile Pro Gln Arg Ala Asn Asp Tyr Ala Ser Leu Ala Leu Ser
 370 375 380
 Ser Leu Ile His Ala Leu Tyr Glu Leu Glu Ser Tyr Ala Val Ala Arg
 385 390 395 400
 Leu Val Thr Lys Glu Ser Lys Pro Pro Met Leu Val Leu Leu Ala Pro
 405 410 415
 Ser Ile Glu Ala Asp Tyr Glu Cys Leu Ile Glu Val Gln Leu Pro Phe
 420 425 430
 Ala Glu Asp Val Arg Ser Tyr Arg Phe Pro Pro Leu Asp Lys Ile Ile
 435 440 445
 Thr Val Ser Gly Lys Val Val Thr Glu His Arg Asn Leu Pro Ser Val
 450 455 460
 Ala Leu Lys Asp Ala Met Ser Asn Tyr Val Asp Ser Met Asp Phe Val
 465 470 475 480
 Thr Thr Asn Asp Glu Gly Gln Ala Thr Asp Asp Leu Pro Ile Asp Glu
 485 490 495
 Ser Phe Ser Pro Leu Leu His Arg Ile Glu Ser Ala Val Arg Tyr Arg
 500 505 510
 Ala Val His Pro Asn Asp Pro Val Leu Asp Pro Ser Glu Arg Leu Thr
 515 520 525

Glu Phe Ala His Pro Ser Glu Asp Met Val Lys Asn Ser Lys Ser His
530 535 540

Leu Glu Lys Leu Met Ser Ile Ala Asp Val Lys Lys Val Pro Pro Lys
545 550 555 560

Thr Lys Gly Arg Lys Arg Gln Arg Glu Thr Glu Lys Pro Leu Ser Gly
565 570 575

Leu Asp Val Asp Ala Leu Leu Ser Leu Glu Pro Lys Arg Thr Lys Ile
580 585 590

Ser Thr Glu Asn Ala Ile Pro Glu Phe Lys Gln Thr Leu Ser Arg Ala
595 600 605

Glu Asn Ile Asp Ala Ile His Asp Ala Val Gln Gln Met Ala Lys Ile
610 615 620

Ile Glu Ser Gln Ile Thr His Ser Leu Gly His Ser Asn Tyr Asp Arg
625 630 635 640

Val Ile Glu Gly Leu Gly Thr Met Arg Glu Glu Leu Val Asp Tyr Glu
645 650 655

Glu Pro Ala Val Tyr Asn Asp Phe Val Arg Gln Leu Lys Gly Lys Met
660 665 670

Leu Arg Glu Glu Leu Gly Gly Asp Arg Arg Glu Leu Trp Trp Phe Val
675 680 685

Arg Lys Gly Lys Leu Gly Leu Ile Gly Lys Ser Glu Val Asp Ser Ser
690 695 700

Ala Val Glu Glu Gln Glu Ala Gln Glu Phe Leu Ala Pro Asn
705 710 715